

Lee, B.
1016235c7
Seq. ID 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2005, 21:41:13 ; Search time 165 Seconds
(without alignments)
731.329 Million cell updates/sec

Title: US-10-623-567a-1

Perfect score: 1573

Sequence: 1 MANNDVLRLEQKGAEADQ.....FEVKGKGVCRQATMSNSGIK 312

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1573	100.0	312	5	Abb07442 Human p43
2	1573	100.0	312	6	Aao29575 Human Pc2
3	1573	100.0	312	8	Adh74487 Human wou
4	1573	100.0	312	8	Adp85653 Human end
5	1573	100.0	328	4	Aab63244 Human bre
6	1343	85.4	310	2	Aar72577 Mouse EMA
7	831	52.8	166	6	Abu10452 Immunolog
8	831	52.8	166	8	Ad80906 Mammalian
9	823	52.3	166	2	Aaw14561 Endotheli
10	709	45.1	147	6	Abu10250 Immunolog
11	709	45.1	147	8	Ad80904 Mammalian
12	671	42.7	294	4	Abb59210 Drosophil
13	522.5	33.2	280	7	Abm74361 DNA clone
14	522.5	33.2	289	7	Abm73655 DNA clone
15	516	32.8	108	6	Abu10451 Immunolog
16	510.5	32.5	659	5	Ad80905 Mammalian
17	510.5	32.5	659	5	Aae19811 Corn p012
18	507	32.2	95	8	Adn99968 Novel hum
19	499	31.7	797	8	Adn73157 Thale cre
20	451	28.7	536	4	Ab47611 Human ful
21	451	28.7	536	5	Aae13487 Human tyr
22	451	28.7	536	6	Abu72380 Human ful
23	450	28.6	528	7	Adf76697 Novel hum
24	450	28.6	528	8	Adn05830 Antipsori
25	450	28.6	528	8	Adq65849 Novel hum

ALIGNMENTS

RESULT 1

ABB07442
ID ABB07442 standard; protein; 312 AA.

AC ABB07442;

DT 23-APR-2002 (first entry)

DS Human p43 polypeptide.

XX Human; p43; cytostatic; anti-tumour; anti-angiogenic; EMAP II; cytokine;

KW Chemotaxis.

OS Homo sapiens.

Key	Location/Qualifiers
Domain	1..146
Region	/note= "N-terminal domain"
Region	10..21
Region	/note= "beta1 strand"
Region	28..34
Region	/note= "beta2 strand"
Region	40..46
Region	/note= "beta3 strand"
Region	53..56
Region	/note= "alpha 1 helix"
Region	59..66
Region	/note= "beta4 strand"
Region	70..72
Region	/note= "beta5i strand"
Region	75..77
Region	/note= "beta6i strand"
Region	79..85
Region	/note= "beta7 strand"
Region	90..92
Region	/note= "beta8 strand"
Region	103..106
Region	/note= "beta9 strand"
Region	119..123
Region	/note= "alpha 2 helix"
Region	124..130
Region	/note= "alpha 3 helix"
Region	132..134
Region	/note= "beta10 strand"
Region	140..142
Region	/note= "beta11 strand"
Domain	147..312
	/note= "C-terminal domain"

XX WO200195927-A1.
 XX 20-DEC-2001.
 XX 14-JUN-2000; 2000WO-KR000630.
 XX 14-JUN-2000; 2000WO-KR000630.
 XX (IMAG-) IMAGENE CO LTD.
 XX Kim S, Ko Y, Kim YS, Jo YJ;
 XX WPI; 2002-098017/13.
 XX N-PSDB; ABA94640.
 XX Novel anti-tumor and anti-angiogenic agent of p43 comprises N-terminal
 PT domain and C-terminal domain containing eleven beta-strands forming a
 PT structural core and three flanking alpha-helices.
 XX Claim 1; Fig 1; 35pp; English.
 XX The invention provides an anti-tumor and anti-angiogenic agent of p43
 CC consisting of two domains, the N-terminal domain (146 amino acids) and C-
 CC terminal domain (166 amino acids) containing 11 beta-strands forming a
 CC structural core and 3 flanking alpha-helices. p43 is useful as an anti-
 CC tumor and anti-angiogenic agent. p43 and its C-terminal cytokine domain
 CC (SMAP II) induce regression of fibrosarcoma in immunocompromised mouse
 CC while its N-terminal domain does not. p43 is a potent cytokine as
 CC determined by the induction of tumour necrosis factor-alpha (TNF-alpha),
 CC interleukin-6 (IL-6), IL-8 and matrix metalloproteinase-9 or by its
 CC activity of chemotaxis. The present sequence represents the human p43
 CC polypeptide
 XX Sequence 312 AA;
 SQ
 Query Match 100.0%; Score 1573; DB 5; Length 312;
 Best Local Similarity 100.0%; Pred. No. 1.6e-135;
 Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MANNDVAVLKEQKGAADQIIIEYLKQVSLKKEKAILQATLREKKLRYENAKLKEIE 60
 DB 1 MANNDVAVLKEQKGAADQIIIEYLKQVSLKKEKAILQATLREKKLRYENAKLKEIE 60
 QY 61 ELKQELIQAEIQNGVQKIAPPSTPLHANSWSENVIQSTAVTVSSGTKEQIKGGTGE 120
 DB 61 ELKQELIQAEIQNGVQKIAPPSTPLHANSWSENVIQSTAVTVSSGTKEQIKGGTGE 120
 QY 121 KKAKEIEKKGEKKKQKQSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEVD 180
 DB 121 KKAKEIEKKGEKKKQKQSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEVD 180
 QY 181 VGEIAPRTVTVSGLVNHPLEQMNRMVILLCNLKPARKRGVLQAMVCMCASSPEKIEILA 240
 DB 181 VGEIAPRTVTVSGLVNHPLEQMNRMVILLCNLKPARKRGVLQAMVCMCASSPEKIEILA 240
 QY 241 PPNQSVPGDRITTFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVCATYKGVPEVKGKV 300
 DB 241 PPNQSVPGDRITTFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVCATYKGVPEVKGKV 300
 QY 301 CRAFTMSNSGIK 312
 DB 301 CRAFTMSNSGIK 312
 RESULT 2
 AAO29575
 ID AAO29575 standard; protein; 312 AA.
 XX AAO29575;
 AC AAO29575;
 XX 27-AUG-2003 (first entry)
 XX

DE Human Pc240 protein.
 XX Human; differentially regulated protein; prevention; therapy; vaccine;
 KW prostate cancer; endothelial monocyte activating polypeptide II;
 KW gene therapy; Pc240.
 XX Homo sapiens.
 XX WO2003040331-A2.
 XX 15-MAY-2003.
 XX 07-NOV-2002; 2002WO-US035563.
 XX 07-NOV-2001; 2001US-0331041P.
 PR 07-NOV-2001; 2001US-0331042P.
 PR 18-DEC-2001; 2001US-0340251P.
 PR 07-JAN-2002; 2002US-0344791P.
 XX (ORIG-) ORIGENE TECHNOLOGIES INC.
 XX Sun Z, Li X, Jay G, Kovacs KF, Fan W;
 PI WPI; 2003-449451/42.
 DR N-PSDB; AAL60070.
 XX New polynucleotide for diagnosing, staging, monitoring, prognosticating,
 PT preventing or treating, or determining the predisposition to, diseases or
 PT conditions such as prostate cancer, and for research or forensic science.
 XX Disclosure; Page 183-184; 100pp; English.
 XX The present invention relates to novel differentially regulated genes and
 CC polypeptides encoded by them. Sequences of the invention are useful in
 CC diagnosing, staging, monitoring, prognosticating, preventing, treating or
 CC determining the predisposition to diseases or conditions such as prostate
 CC cancer. They may be used as molecular markers, drug targets, vaccines, in
 CC gene therapy, research, clinical medicine or forensic science. The
 CC present sequence is a differentially regulated prostate protein
 CC (endothelial monocyte activating polypeptide II), Pc240
 XX Sequence 312 AA;
 SQ
 Query Match 100.0%; Score 1573; DB 6; Length 312;
 Best Local Similarity 100.0%; Pred. No. 1.6e-135;
 Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MANNDVAVLKEQKGAADQIIIEYLKQVSLKKEKAILQATLREKKLRYENAKLKEIE 60
 DB 1 MANNDVAVLKEQKGAADQIIIEYLKQVSLKKEKAILQATLREKKLRYENAKLKEIE 60
 QY 61 ELKQELIQAEIQNGVQKIAPPSTPLHANSWSENVIQSTAVTVSSGTKEQIKGGTGE 120
 DB 61 ELKQELIQAEIQNGVQKIAPPSTPLHANSWSENVIQSTAVTVSSGTKEQIKGGTGE 120
 QY 121 KKAKEIEKKGEKKKQKQSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEVD 180
 DB 121 KKAKEIEKKGEKKKQKQSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEVD 180
 QY 181 VGEIAPRTVTVSGLVNHPLEQMNRMVILLCNLKPARKRGVLQAMVCMCASSPEKIEILA 240
 DB 181 VGEIAPRTVTVSGLVNHPLEQMNRMVILLCNLKPARKRGVLQAMVCMCASSPEKIEILA 240
 QY 241 PPNQSVPGDRITTFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVCATYKGVPEVKGKV 300
 DB 241 PPNQSVPGDRITTFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVCATYKGVPEVKGKV 300
 QY 301 CRAFTMSNSGIK 312
 DB 301 CRAFTMSNSGIK 312
 RESULT 3

Db 121 KKAKEKIEKGEKKQKQSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEVD 180
 Qy 181 VGEIAPRTVTVSGLVNHVPLEQMNRMVILLCNLKPAMRGVLSQAMVMCASSPEKIEILA 240
 Db 181 VGEIAPRTVTVSGLVNHVPLEQMNRMVILLCNLKPAMRGVLSQAMVMCASSPEKIEILA 240
 Qy 241 PPNCSVPGDRITFDAPFGEPPDKELNPKKTIWEIQPDLHTNDECVAATYKGVPEVKGKV 300
 Db 241 PPNCSVPGDRITFDAPFGEPPDKELNPKKTIWEIQPDLHTNDECVAATYKGVPEVKGKV 300
 Qy 301 CRAFTMSNSGIK 312
 Db 301 CRAFTMSNSGIK 312
 RESULT 5
 AAB63244
 ID AAB63244 standard; protein; 328 AA.
 XX
 AC AAB63244;
 XX
 XX
 XX 26-MAR-2001 (first entry)
 XX Human breast cancer associated antigen protein sequence SEQ ID NO:606.
 XX Human; breast cancer; gastric cancer; prostate cancer; diagnosis;
 KW cancer associated antigen; cytostatic; cancer vaccine.
 XX
 XX Homo sapiens.
 XX W0200073801-A2.
 XX
 PD 07-DEC-2000.
 XX
 XX 26-MAY-2000; 2000WO-US014749.
 XX
 XX 28-MAY-1999; 99US-0136526P.
 PR 10-SEP-1999; 99US-0153454P.
 XX
 XX (LUDW-) LUDWIG INST CANCER RES.
 XX
 XX Obata Y;
 PI
 XX WPI; 2001-025274/03.
 XX
 XX Nucleic acids encoding breast, gastric and prostate cancer associated
 PT antigen precursors, useful for diagnosing and treating a condition
 PT characterized by expression of an abnormal amount of a protein, e.g.
 PT cancer.
 XX
 XX Example 1; Page 478; 799pp; English.
 XX
 XX AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014
 CC represent nucleotide sequences encoding human breast, gastric and
 CC prostate cancer associated antigen precursors (CAAP) respectively.
 CC AAB63232 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970
 CC represent human breast, gastric and prostate CAAP protein sequence
 CC respectively. CAAPs have cytostatic activity and can be used in the
 CC reduction of cancer vaccines. The human CAAP proteins, peptides, nucleic
 CC acids or anti-CAAP antibodies are useful for diagnosing and treating a
 CC condition characterised by expression of an abnormal amount of a protein,
 CC e.g. cancer
 XX
 SQ Sequence 328 AA;
 Query Match 100.0%; Score 1573; DB 4; Length 328;
 Best Local Similarity 100.0%; Pred. No. 1.7e-135;
 Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 61 ELKQELIQAEIQNGVKOIAFPSPGTPHANSMVSENVISTAVTTVSSGTEKQIKGGTGDE 120
 Db 77 ELKQELIQAEIQNGVKOIAFPSPGTPHANSMVSENVISTAVTTVSSGTEKQIKGGTGDE 136
 Qy 121 KKAKEKIEKGEKKQKQSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEVD 180
 Db 137 KKAKEKIEKGEKKQKQSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEVD 196
 Qy 181 VGEIAPRTVTVSGLVNHVPLEQMNRMVILLCNLKPAMRGVLSQAMVMCASSPEKIEILA 240
 Db 197 VGEIAPRTVTVSGLVNHVPLEQMNRMVILLCNLKPAMRGVLSQAMVMCASSPEKIEILA 256
 Qy 241 PPNCSVPGDRITFDAPFGEPPDKELNPKKTIWEIQPDLHTNDECVAATYKGVPEVKGKV 300
 Db 257 PPNCSVPGDRITFDAPFGEPPDKELNPKKTIWEIQPDLHTNDECVAATYKGVPEVKGKV 316
 Qy 301 CRAFTMSNSGIK 312
 Db 317 CRAFTMSNSGIK 328
 RESULT 6
 AAR72577
 ID AAR72577 standard; protein; 310 AA.
 XX
 AC AAR72577;
 XX
 DT 25-MAR-2003 (revised)
 DT 29-SEP-1995 (first entry)
 XX
 DE Mouse EMAP11.
 XX
 XX EMAP11; endothelial monocyte activating polypeptide II; chemotaxis;
 KW inflammation; tissue factor; tumor; cancer; therapy; methA; sarcoma.
 XX
 OS Mus musculus.
 XX
 XX W09509180-A1.
 XX
 PD 06-APR-1995.
 XX
 XX 29-SEP-1994; 94WO-US011085.
 PF
 XX 29-SEP-1993; 93US-00129456.
 PR
 XX (UYCO) UNIV COLUMBIA NEW YORK.
 XX
 XX Stern DM, Clauss M, Kao J, Kayton M, Libutti SK;
 PI
 XX WPI; 1995-147389/J9.
 DR
 DR N-PSDB; AAQ86718.
 XX
 XX New endothelial monocyte activating polypeptide II - induces chemotaxis,
 PT inflammation and tissue factor, useful for treating tumours, also related
 PT antibodies, DNA and active fragments.
 XX
 PS Disclosure; Fig 4; 180pp; English.
 XX
 CC A mouse methA sarcoma cDNA library was screened with a probe based on the
 CC N-terminal sequence of mouse EMAP11. Overlapping clones were combined to
 CC obtain a contiguous full-length sequence (given in AAQ86718) encoding a 33
 CC kDa protein (AAR72577). Recombinant EMAP11 was expressed in E. coli.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 310 AA;
 Query Match 85.4%; Score 1343; DB 2; Length 310;
 Best Local Similarity 85.9%; Pred. No. 2e-114;
 Matches 269; Conservative 13; Mismatches 27; Indels 4; Gaps 3;
 Qy 1 MANNDVLRLEQKGAEDQIIEYLRKQVSLKKEKAILQATLRREKRLRVENAKLKEIE 60
 Db 17 MANNDVLRLEQKGAEDQIIEYLRKQVSLKKEKAILQATLRREKRLRVENAKLKEIE 76

Db 1 MATNDVLRLEQKGAEDQIIEYLKQVALLKEKAILQATMRBEKKLRVNAKLKKEIE 60
QY 61 ELKQELIOAEIQTGKQVAFPSGTPHANSMVSENVIOSTAV-TTVSSGTKEQIKGGTGD 119
Db 61 ELKQELILAEIHNGVEQVRVLSPLQTNCTASGVQSPVATSPATKEQIK--AGE 118
QY 120 EKKAKEIEKKEKKEKQSIAGSADSKPIIDVSRDLRIGCIITARKHPDADSLYYVEEV 179
Db 119 EKKVKEKTEKKEKKE--KQSAASATDSKPIDASRLDLRIGCIITAKKHPDADSLYYVEEV 177
QY 180 DVGEIAPRTVTVSSGLVNHVPLEQMQNRMVILLCNLPAKMRGVLQAMVMCASSPEKTEIL 239
Db 178 DVGEAAPRTVTVSSGLVNHVPLEQMQNRMVILLCNLPAKMRGVLQAMVMCASSPEKTEIL 237
QY 240 APPNGSVPGDRITFDAPFGEPDKELNPKKIWEQIQDPLHTNDECVATYKGVPEVKKG 299
Db 238 APPNGSVPGDRITFDAPFGEPDKELNPKKIWEQIQDPLHTNAECVATYKGAPEVKKG 297
QY 300 VCRAQTMSNGIK 312
Db 298 VCRAQTMSNGIK 310
RESULT 7
ABU10452
ID ABU10452 standard; protein; 166 AA.
AC ABU10452;
XX
XX
DT 01-AUG-2003 (first entry)
XX
XX
DE Immunological enhancement agent p43 (91-256).
XX
XX
KW Immunostimulant; cytokine agonist; p43; cytokine; interleukin-8; TNF;
KW tumour necrosis factor.
XX
XX
OS Mammalia.
XX
XX
PN US2003004309-A1.
XX
XX
PD 02-JAN-2003.
XX
XX
PF 16-AUG-2001; 2001US-00930169.
XX
XX
PR 05-JUN-2001; 2001KR-00031310.
XX
XX
PA (KIMS/) KIM S.
PA (KOYY/) KO Y.
PI Kim S, Ko Y;
XX
XX
WPI; 2003-447359/42.
XX
XX
DR New immunological enhancement agent comprising an N-terminal peptide of
PT p43, useful for increasing the amount of tumor necrosis factor and
PT interleukin-8 to improve the immune response.
XX
XX
PS Claim 3; Page 5; 12pp; English.
XX
XX
CC The present sequence represents an immunological enhancement agent
CC comprising an N-terminal peptide of p43. The peptide can act as a
CC cytokine to increase the amount of tumour necrosis factor (TNF) and
CC interleukin-8 useful for improving an immune response and used as an
CC immunological enhancement agent. The present sequence represents the
CC amino acid sequence of the immunological enhancement agent p43 (91-256)
XX
XX
SQ Sequence 166 AA;
Query Match 52.8%; Score 831; DB 6; Length 166;
Best Local Similarity 100.0%; Pred. No. 7.8e-68;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 91 MVSENVIOSTAVTTVSSGTKEQIKGGTGDKEKAKEIEKKKEKQKQSIAGSADSKPI 150

Db 1 MVSENVIOSTAVTTVSSGTKEQIKGGTGDKEKAKEIEKKKEKQKQSIAGSADSKPI 60
QY 151 DVSRDLRIGCIITARKHPDADSLYYVEVDVGEIAPRTVTVSSGLVNHVPLEQMQNRMVILL 210
Db 61 DVSRDLRIGCIITARKHPDADSLYYVEVDVGEIAPRTVTVSSGLVNHVPLEQMQNRMVILL 120
QY 211 CNLPAKMRGVLQAMVMCASSPEKTEILAPPNGSVPGDRITFDAP 256
Db 121 CNLPAKMRGVLQAMVMCASSPEKTEILAPPNGSVPGDRITFDAP 166
RESULT 8
ADS80906
ID ADS80906 standard; protein; 166 AA.
XX
XX
AC ADS80906;
XX
XX
DT 16-DEC-2004 (first entry)
XX
XX
DE Mammalian p43(91-256) protein.
XX
XX
KW Immune response; p43; apoptotic disorder; cancer; cytostatic;
KW immunostimulant; cytokine-agonist.
XX
XX
OS Mammalia.
XX
XX
PN US2004185060-A1.
XX
XX
PD 23-SEP-2004.
XX
XX
PF 14-APR-2004; 2004US-00823730.
XX
XX
PR 05-JUN-2001; 2001KR-00031310.
PR 16-AUG-2001; 2001US-00930169.
XX
XX
PA (IMAG-) IMAGENE CO LTD.
XX
XX
PI Kim S, Ko Y;
XX
XX
WPI; 2004-689153/67.
XX
XX
DR Enhancing an immune response using an immunological enhancement agent
PT having the N-terminal domain of the p43 protein, useful in apoptotic
PT disorders such as cancer.
XX
XX
PS Disclosure; SEQ ID NO 3; 12pp; English.
XX
XX
CC The present invention relates to a method of enhancing an immune
CC response. The method involves administering an immunological enhancement
CC agent having the N-terminal domain of p43 protein to a cell or tissue.
CC The invention is useful for enhancing an immune response with an
CC immunological enhancement agent in apoptotic disorders such as cancer.
XX
XX
SQ Sequence 166 AA;
Query Match 52.8%; Score 831; DB 8; Length 166;
Best Local Similarity 100.0%; Pred. No. 7.8e-68;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 91 MVSENVIOSTAVTTVSSGTKEQIKGGTGDKEKAKEIEKKKEKQKQSIAGSADSKPI 150
Db 1 MVSENVIOSTAVTTVSSGTKEQIKGGTGDKEKAKEIEKKKEKQKQSIAGSADSKPI 60
QY 151 DVSRDLRIGCIITARKHPDADSLYYVEVDVGEIAPRTVTVSSGLVNHVPLEQMQNRMVILL 210
Db 61 DVSRDLRIGCIITARKHPDADSLYYVEVDVGEIAPRTVTVSSGLVNHVPLEQMQNRMVILL 120
QY 211 CNLPAKMRGVLQAMVMCASSPEKTEILAPPNGSVPGDRITFDAP 256
Db 121 CNLPAKMRGVLQAMVMCASSPEKTEILAPPNGSVPGDRITFDAP 166

```

RESULT 9
AAW14561
ID AAW14561 standard; protein; 166 AA.
XX
AC AAW14561;
XX
XX
DT 01-DEC-1997 (first entry)
XX
DE Endothelial monocyte activating polypeptide II.
XX
KW EMAP-II; inhibitor; endothelial cell formation; blood vessel;
KW retinopathy; tumour; subcutaneous; intraperitoneal; intravenous;
KW intracranial; intratumoural; carcinoma; glioblastoma;
KW positive pressure microinfusion; aortic cell; angiogenesis; eye disease;
KW diabetes; sickle cell anaemia; prematurity;
KW age-related macular degeneration.
XX
OS Mus musculus.
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /label= Ser, Met, Gly
FT FT Misc-difference 15
FT FT /label= Cys, Arg
XX
XX
FN W09710841-A1.
XX
XX
PD 27-MAR-1997.
XX
XX
PF 18-SEP-1996; 96WO-US015007.
XX
XX
PR 18-SEP-1995; 95US-0003898P.
XX
XX
PA (UYCO ) UNIV COLUMBIA NEW YORK.
XX
XX
PI Stern D, Schwarz M;
XX
XX
WPI; 1997-202617/18.
XX
XX
PT Treatment of tumours with endothelial monocyte activating peptide II -
PT also used to inhibit growth of endothelial cells and formation of blood
PT vessels, e.g. in retinopathy.
XX
XX
PS Claim 13; Page 73; 104pp; English.
XX
XX
CC A method has been developed for the treatment of tumours. The method
CC involves subcutaneous, intraperitoneal, intravenous, intracranial or
CC intratumoural administration of an endothelial monocyte activating
CC polypeptide II (EMAP-II), or a EMAP-II-derived polypeptide. The present
CC sequence represents murine EMAP-II which can be used to produce the EMAP-
CC II-derived polypeptide as long as it contains at least ninety percent
CC homology to the present sequence. The method is especially used to treat
CC carcinoma (administered intraperitoneally) or glioblastoma (administered
CC intratumourally by positive pressure microinfusion). Inhibition of
CC endothelial cell growth is particularly applied to aortic cells and
CC inhibition of angiogenesis to treatment of eye diseases associated with
CC excessive blood vessel formation, especially retinopathy (diabetic,
CC related to sickle cell anaemia, retinopathy of prematurity or age-related
CC macular degeneration). Intraperitoneal administration allows tumours too
CC small (not over 2 mm in diameter) for intratumoural injection to be
CC treated before they grow larger
XX
XX
SQ Sequence 166 AA;
Query Match 52.3%; Score 823; DB 2; Length 166;
Best Local Similarity 93.9%; Pred. No. 4.2e-67;
Matches 155; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 148 KPIDSRLDLRIGCIITARKHPDADSLYVEEDVGEIAPRTTVSGLVNHPLEQMQRNV 207
DB 2 KPIDASRLDLRIGXIVTAKHPDADSLYVEEDVGEIAPRTTVSGLVNHPLEQMQRNV 61

RESULT 10
ABU10250
ID ABU10250 standard; protein; 147 AA.
XX
AC ABU10250;
XX
XX
DT 01-AUG-2003 (first entry)
XX
DE Immunological enhancement agent p43 (1-147).
XX
KW Immunostimulant; cytokine agonist; p43; cytokine; interleukin-8; TNF;
KW tumour necrosis factor.
XX
OS Mammalia.
XX
XX
PN US2003004309-A1.
XX
XX
PD 02-JAN-2003.
XX
XX
PF 16-AUG-2001; 2001US-00930169.
XX
XX
PR 05-JUN-2001; 2001KR-00031310.
XX
XX
PA (KIMS/) KIM S.
PA (KOYY/) KO Y.
XX
XX
PI Kim S, Ko Y;
XX
XX
WPI; 2003-447359/42.
XX
XX
PT New immunological enhancement agent comprising an N-terminal peptide of
PT p43, useful for increasing the amount of tumor necrosis factor and
PT interleukin-8 to improve the immune response.
XX
XX
PS Claim 1; Page 4; 12pp; English.
XX
XX
CC The present sequence represents an immunological enhancement agent
CC comprising an N-terminal peptide of p43. The peptide can act as a
CC cytokine to increase the amount of tumor necrosis factor (TNF) and
CC interleukin-8 useful for improving an immune response and used as an
CC immunological enhancement agent. The present sequence represents the
CC amino acid sequence of the immunological enhancement agent p43 (1-147)
XX
XX
SQ Sequence 147 AA;
Query Match 45.1%; Score 709; DB 6; Length 147;
Best Local Similarity 100.0%; Pred. No. 1e-56;
Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANNDVLRKLEQKGAADQIIIEYLKQVSLLEKAILQATLREKKLRVENAKLKEIE 60
DB 1 MANNDVLRKLEQKGAADQIIIEYLKQVSLLEKAILQATLREKKLRVENAKLKEIE 60

QY 61 ELKQELIQAEIQNGVKQIAPPSGTPHLHANSVENVIOSTAVTTVSSGTKEQIKGGTGDE 120
DB 61 ELKQELIQAEIQNGVKQIAPPSGTPHLHANSVENVIOSTAVTTVSSGTKEQIKGGTGDE 120

QY 121 KKAKEKIEKKGEKKKQSQSIAGSADS 147
DB 121 KKAKEKIEKKGEKKKQSQSIAGSADS 147

RESULT 11
ADS80904

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ID ADS80904 standard; protein; 147 AA.
 AC ADS80904;
 XX
 DT 16-DEC-2004 (first entry)
 XX
 DE Mammalian p43(1-147) protein.
 XX
 KW Immune response; p43; apoptotic disorder; cancer; cytostatic;
 KW immunostimulant; cytokine-agonist.
 XX
 OS Mammalia.
 OS
 PN US2004185060-A1.
 PN
 PD 23-SEP-2004.
 PD
 XX 14-APR-2004; 2004US-00823730.
 XX
 PF 05-JUN-2001; 2001KR-00031310.
 PF
 PR 16-AUG-2001; 2001US-00930169.
 PR
 XX (IMAG-) IMAGENE CO LTD.
 XX
 PA Kim S, Ko Y;
 PA
 PI WPI; 2004-689153/67.
 PI
 DR Enhancing an immune response using an immunological enhancement agent
 DR having the N-terminal domain of the p43 protein, useful in apoptotic
 PT disorders such as cancer.
 PT
 PT Disclosure; SEQ ID NO 1; 12pp; English.
 PS
 XX The present invention relates to a method of enhancing an immune
 XX response. The method involves administering an immunological enhancement
 CC agent having the N-terminal domain of p43 protein to a cell or tissue.
 CC The invention is useful for enhancing an immune response with an
 CC immunological enhancement agent in apoptotic disorders such as cancer.
 CC The present sequence is the mammalian p43(1-147) protein.
 XX
 SQ Sequence 147 AA;
 Query Match 45.1%; Score 709; DB 8; Length 147;
 Best Local Similarity 100.0%; Pred. No. 1e-56;
 Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 1 MANNDVLRLEQKGAADQIIIEYLKQOVSLLEKAILQATLREKKLRVENAKLKEIE 60
 Qy 61 ELKQELIQAEIQNGVKQIAFSPGTPPLHANSMVSENVIOSTAVTTVSSGKQIKGGTGDE 120
 Db 61 ELKQELIQAEIQNGVKQIAFSPGTPPLHANSMVSENVIOSTAVTTVSSGKQIKGGTGDE 120
 Qy 121 KKAKEKLEKKEKKEKQOQSTAGSADS 147
 Db 121 KKAKEKLEKKEKKEKQOQSTAGSADS 147
 RESULT 12
 ABB59210
 ID ABB59210 standard; protein; 294 AA.
 XX
 AC ABB59210;
 XX
 DT 26-MAR-2002 (first entry)
 DT
 DE Drosophila melanogaster polypeptide SEQ ID NO 4422.
 DE
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX

OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 PD
 XX 23-MAR-2001; 2001WO-US009231.
 XX
 PF 23-MAR-2000; 2000US-0191637P.
 PF
 PR 11-JUL-2000; 2000US-00614150.
 PR
 XX (PEKE) PE CORP NY.
 XX
 PA Venter JC, Adams M, Li PWD, Myers EW;
 PA
 PI WPI; 2001-656860/75.
 PI
 DR N-PSDB; ABL03313.
 DR
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 XX genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions.
 PT
 PT Disclosure; SEQ ID NO 4422; 21pp + Sequence Listing; English.
 PS
 XX The invention relates to an isolated nucleic acid detection reagent
 XX capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABU16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 294 AA;
 Query Match 42.7%; Score 671; DB 4; Length 294;
 Best Local Similarity 44.9%; Pred. No. 8.6e-53;
 Matches 141; Conservative 57; Mismatches 88; Indels 28; Gaps 5;
 Qy 6 AVLKRLQKGAADQIIIEYLKQOVSLLEKAILQATLREKKLRVENAKLKEIEELKQK 65
 Db 2 ADLQIQASNNRERAEALINSIEAETISGQQ-----QLVERQKQELIKENAAKAEVAAALQ 57
 Qy 66 LIQAEIQNGVKQIAFP-----SGTPPLHANSMVSENVIOSTAVTTVSSGKQIKGGTG 118
 Db 58 LVQLELRNGKKQIPVPGARGFCTSAAPV-----VMPAAGAPATAAPAA 102
 Qy 119 DEKKAKEKLEKKEKKEKQOQSTAGSADSKPIDVSRDLRLRIGCIITARKHPDADSLYVEE 178
 Db 103 -PKPAKEPKKEKKEKPAAEKPA-AAPEAPVDVGRDLRVGKIVEGRHPDADSLYLEK 160
 Qy 179 VDVGGEIAPRTVSGLVNHPLEOMQNRVILLCNLKPAPKRGVLSQAMVMCASSPEKIEI 238
 Db 161 IDCCEAAPRTVSGLVKFPVPLEENRLLVVMCNLKPAPKRGVTSAMVMCASTPEKVEV 220
 Qy 239 LAPNGSVPGDRITFDAPFGPEPKELNPKKIWEQIOPDLHTNDECATYKGVPEVKGK 298
 Db 221 LSPAPGAPVPGDLVHCEGYPRQPDQALNPKPKKIFESCAPDLKTNGLVACYGAALHVPKG 280
 Qy 299 GVCRAQTMNSNGIK 312
 Db 281 GNVVAQILKNVVK 294
 RESULT 13
 ABB74361
 ID ABB74361 standard; protein; 280 AA.
 XX
 AC ABB74361;
 XX
 DT 17-OCT-2003 (first entry)
 DT

XX 01-AUG-2003 (first entry)
DT Immunological enhancement agent p43 (1-108).
DE Immunological enhancement agent p43 (1-108).
XX Immunostimulant; cytokine agonist; p43; cytokine; interleukin-8; TNF;
KW tumour necrosis factor.
XX Mammalia.
OS
XX US2003004309-A1.
FN
XX 02-JAN-2003.
PD
XX 16-AUG-2001; 2001US-00930169.
PF
XX 05-JUN-2001; 2001KR-000311310.
PR
XX (KIMS/) KIM S.
PA (KOYY/) KO Y.
XX
XX Kim S, Ko Y;
PI
XX WPI; 2003-447359/42.
DR
XX New immunological enhancement agent comprising an N-terminal peptide of
PT p43, useful for increasing the amount of tumor necrosis factor and
PT interleukin-8 to improve the immune response.
XX
XX Claim 2; Page 5; 12pp; English.
PS
XX The present sequence represents an immunological enhancement agent
XX comprising an N-terminal peptide of p43. The peptide can act as a
CC cytokine to increase the amount of tumour necrosis factor (TNF) and
CC interleukin-8 useful for improving an immune response and used as an
CC immunological enhancement agent. The present sequence represents the
CC amino acid sequence of the immunological enhancement agent p43 (1-108)
XX
XX Sequence 108 AA;
SQ
Query Match 32.8%; Score 516; DB 6; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.4e-39;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MANNDVLTKRLEQKGAEDQIIEYLKQOVSLKKEKAILQATLREKKLRVENAKLKEIE 60
Qy 61 ELKQELIQAEIQGVKQIAFPSTPLHANSMVSENVISQSTAVTTVSSG 108
Db 61 ELKQELIQAEIQGVKQIAFPSTPLHANSMVSENVISQSTAVTTVSSG 108
Search completed: August 3, 2005, 21:54:21
Job time : 168 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2005, 21:47:49 ; Search time 42 Seconds
(without alignments)
554.536 Million cell updates/sec

US-10-623-567A-1

Title:

Perfect score: 1573

Sequence:

1 MANNDVLRLEQKGAEADQ.....FEVKGKVCRAQTWNSGIK 312

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1568	99.7	312	3	US-08-360-821B-36
2	1568	99.7	312	4	US-09-851-026-36
3	1568	99.7	320	4	US-09-949-016-7144
4	1510	96.0	310	1	US-08-129-456A-37
5	1343	85.4	310	1	US-08-129-456A-36
6	1343	85.4	310	2	US-08-705-868-3
7	1343	85.4	310	3	US-09-123-615-3
8	1343	85.4	310	3	US-08-360-821B-35
9	1343	85.4	310	4	US-09-851-026-35
10	931	59.2	183	3	US-08-483-534A-7
11	835	53.1	166	1	US-08-129-456A-11
12	835	53.1	166	3	US-08-360-821B-11
13	835	53.1	166	4	US-09-851-026-11
14	510.5	32.5	659	3	US-09-392-772-10
15	440.5	28.0	301	2	US-08-705-868-1
16	440.5	28.0	301	3	US-09-123-615-1
17	440.5	28.0	301	4	US-09-919-039-132
18	438.5	27.9	215	4	US-09-248-796A-19812
19	429.5	27.3	168	3	US-08-483-534A-2
20	410.5	26.1	492	4	US-09-949-016-10567
21	235	14.9	174	4	US-09-248-796A-19813
22	227	14.4	720	4	US-09-328-352-4765
23	188.5	12.0	674	4	US-09-107-532A-6201
24	186.5	11.9	648	1	US-08-451-715A-4
25	184	11.7	703	4	US-09-902-540-10686
26	182.5	11.6	111	4	US-09-489-039A-9293
27	174.5	11.1	493	4	US-09-134-000C-4034

28	157	10.0	665	3	US-08-844-059-2	Sequence 2, Appli
29	157	10.0	665	3	US-09-431-202-2	Sequence 2, Appli
30	152.5	9.7	336	4	US-09-107-433-4916	Sequence 4916, Ap
31	152.5	9.7	679	4	US-09-583-110-2751	Sequence 2751, Ap
32	147	9.3	221	4	US-09-252-991A-21654	Sequence 21654, A
33	136	8.6	716	4	US-09-489-039A-8243	Sequence 8243, Ap
34	134.5	8.6	680	4	US-09-352-991A-17566	Sequence 17566, A
35	129	8.2	690	4	US-09-540-236-3507	Sequence 3507, Ap
36	128	8.1	115	3	US-08-844-059-4	Sequence 4, Appli
37	128	8.1	115	3	US-09-431-202-4	Sequence 4, Appli
38	128	8.1	683	4	US-09-543-681A-5403	Sequence 5403, Ap
39	119.5	7.6	589	4	US-09-543-681A-7643	Sequence 7643, Ap
40	117	7.4	721	3	US-09-134-078-19	Sequence 19, Appli
41	116.5	7.4	414	5	PCT-US93-03077-3	Sequence 3, Appli
42	116.5	7.4	1093	4	US-09-949-016-11535	Sequence 11535, A
43	116.5	7.4	1093	5	PCT-US93-03077-1	Sequence 1, Appli
44	116	7.4	1118	4	US-09-949-016-6596	Sequence 6596, Ap
45	116	7.4	1120	4	US-09-949-016-10404	Sequence 10404, A

ALIGNMENTS

RESULT 1
US-08-360-821B-36
; Sequence 36, Application US/08360821B
; Patent No. 6228837
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Clauss, Matthias
; APPLICANT: Kao, Janet
; APPLICANT: Kayton, Mark
; APPLICANT: Libutti, Steven K
; TITLE OF INVENTION: Endothelial Monocyte Activating
; TITLE OF INVENTION: Polypeptide II: A Mediator Which Activates Host Response
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham, LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.30, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,821B
; FILING DATE: 08-OCT-96
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41735-A-PCT-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 312 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-360-821B-36

Query Match 99.7%; Score 1568; DB 3; Length 312;
Best Local Similarity 99.7%; Pred. No. 2.9e-136;
Matches 311; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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61 ELKQELIOAEIQNGVKQIAPPSTPLHANSMVSENVIOSTAVTVSSGTKEQIKGGTGDE 120
61 ELKQELIOAEIQNGVKQIAPPSTPLHANSMVSENVIOSTAVTVSSGTKEQIKGGTGDE 120
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301 CRAFTMSNSGIK 312
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RESULT 2
US-09-851-026-36
; Sequence 36, Application US/09851026
; Patent No. 6734168
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; Kao, Janet
; Kayton, Mark
; Libutti, Steven K
; TITLE OF INVENTION: Endothelial Monocyte Activating
; Polypeptide II: A Mediator Which Activates Host Response
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham, LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.30, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/851,026
; FILING DATE: 07-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,821
; FILING DATE: 08-OCT-96
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41735-A-PCT-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 312 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-851-026-36

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Query Match 99.7%; Score 1568; DB 4; Length 312;
Best Local Similarity 99.7%; Pred. No. 2.9e-136;
Matches 311; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MANNDVAVLRLEQKGAADQII EYLKQOVSLLEKAILQATLREEKKLRVENAKLKEIE 60
QY 61 ELKQELIOAEIQNGVKQIAPPSTPLHANSMVSENVIOSTAVTVSSGTKEQIKGGTGDE 120
DB 61 ELKQELIOAEIQNGVKQIAPPSTPLHANSMVSENVIOSTAVTVSSGTKEQIKGGTGDE 120
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DB 241 PPNQSVPGDRITFDAPFGEPPDKELNPKKKEIWEQIQPDLHTNDECVATYKGVPEVKGKV 300
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DB 301 CRAFTMSNSGIK 312

RESULT 3
US-09-949-016-7144
; Sequence 7144, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7144
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7144

Query Match 99.7%; Score 1568; DB 4; Length 320;
Best Local Similarity 99.7%; Pred. No. 3e-136;
Matches 311; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 9 MANNDVAVLRLEQKGAADQII EYLKQOVSLLEKAILQATLREEKKLRVENAKLKEIE 68
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DB 69 ELKQELIOAEIQNGVKQIAPPSTPLHANSMVSENVIOSTAVTVSSGTKEQIKGGTGDE 128
QY 121 KKAKEKIEKKGEKKKQOSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEEVD 180
DB 129 KKAKEKIEKKGEKKKQOSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEEVD 188
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DB 189 VGEIAPRTVTVSGLVNHVPLEQMNRMVILLCNLKPAMRGVLSQAMVMCASSPEKIEILA 248

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	Matches 306;	Conservative	0;	Mismatches 3;	Indels 4; Gaps 3;
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1  RESULT 5
2  US-08-129-456A-36
3  Sequence 36, Application US/08129456A
4  Patent No. 5641867
5  GENERAL INFORMATION:
6  APPLICANT: Stern, David M.
7  APPLICANT: Clausen, Matthias
8  APPLICANT: Kao, Janet
9  APPLICANT: Kayton, Mark
10 APPLICANT: Libutti, Steven K.
11 TITLE OF INVENTION: Endothelial-Monocyte Activating
12 TITLE OF INVENTION: Polypeptide II: A Mediator Which
13 TITLE OF INVENTION: Activates Host Response
14 NUMBER OF SEQUENCES: 37
15 CORRESPONDENCE ADDRESS:
16 ADDRESSEE: Cooper & Dunham LLP
17 STREET: 1185 Avenue of the Americas
18 CITY: New York
19 STATE: New York
20 COUNTRY: USA
21 ZIP: 10036
22 COMPUTER READABLE FORM:
23 MEDIUM TYPE: Floppy disk
24 COMPUTER: IBM PC compatible
25 OPERATING SYSTEM: PC-DOS/MS-DOS
26 SOFTWARE: Patent In Release #1.0 Version #1.30
27 CURRENT APPLICATION DATA:
28 APPLICATION NUMBER: US/08/129,456A
29 FILING DATE: 29-SEP-1993
30 CLASSIFICATION: 530
31 ATTORNEY/AGENT INFORMATION:
32 NAME: White, John P.
33 REGISTRATION NUMBER: 28,678
34 REFERENCE/DOCKET NUMBER: 41735
35 TELECOMMUNICATION INFORMATION:
36 TELEPHONE: 212 278 0400
37 TELEFAX: 212 391 0526
38 INFORMATION FOR SEQ ID NO: 36:
39 SEQUENCE CHARACTERISTICS:
40 LENGTH: 310 amino acids
41 TYPE: amino acid
42 TOPOLOGY: linear
43 MOLECULE TYPE: protein
44 US-08-129-456A-36

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[illegible]

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Db 238 APNGSVPGDRITFDAPGPEPKELNPKKKIWEQIQPDLHTNDECVATYKGVPEVKGK 297
Qy 300 VCRAQTMNSNGIK 312
Db 298 VCRAQTMANSNIK 310

RESULT 6

US-08-705-868-3
; Sequence 3, Application US/08705868
; Patent No. 5885798
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Coleman, Roger
; APPLICANT: Au-Young, Janice
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: NOVEL MONOCYTE ACTIVATING CYTOKINE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08705,868
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0117 US
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 310 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 498910
US-08-705-868-3

Query Match 85.4%; Score 1343; DB 2; Length 310;
Best Local Similarity 85.9%; Pred. No. 1.5e-115;
Matches 269; Conservative 13; Mismatches 27; Indels 4; Gaps 3;

Qy 1 MANNDVAVLRLKLEQKGAADQIIEYLKQVSLKKEKAILQATLREKKLRVENAKLKEIE 60
Db 1 MATNDVAVLRLKLEQKGAADQIIEYLKQVALLKEKAILQATMREKKLRVENAKLKEIE 60
Qy 61 ELKQELIQAETQNGVKQIAPPSTGPLHANSVMSENVIQSTAV-TTVSSGTYKEQIKGTTGD 119
Db 61 ELKQELIAEHNGVEQVRVRLSTPLQTNCTASVSVQSPVATTASPAKQIK--AGE 118
Qy 120 EKKAKEIKKKEKKEKQSIAGSADSKPTDVSRLDLRIGCIITARKHPDADSLYVEEV 179
Db 119 EKKVKEKTEKKEKKE-KQSSAAASTDSDPIDASRLDLRIGCIITAKKHPDADSLYVEEV 177

Qy 180 DVGEAPRTVTVSLVNHVPLEQMNRMVLLCNLKPAMRGVLSQAMVMCASSPEKIEIL 239
Db 178 DVGEAPRTVTVSLVNHVPLEQMNRMVLLCNLKPAMRGVLSQAMVMCASSPEKVEIL 237
Qy 240 APNGSVPGDRITFDAPGPEPKELNPKKKIWEQIQPDLHTNDECVATYKGVPEVKGK 299
Db 238 APNGSVPGDRITFDAPGPEPKELNPKKKIWEQIQPDLHTNDECVATYKGVPEVKGK 297
Qy 300 VCRAQTMNSNGIK 312
Db 298 VCRAQTMANSNIK 310

RESULT 7

US-09-123-615-3
; Sequence 3, Application US/09123615
; Patent No. 6090377
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Coleman, Roger
; APPLICANT: Au-Young, Janice
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: NOVEL MONOCYTE ACTIVATING CYTOKINE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09123,615
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/705,868
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0117 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 310 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 498910
US-09-123-615-3

Query Match 85.4%; Score 1343; DB 3; Length 310;
Best Local Similarity 85.9%; Pred. No. 1.5e-115;
Matches 269; Conservative 13; Mismatches 27; Indels 4; Gaps 3;

Qy 1 MANNDVAVLRLKLEQKGAADQIIEYLKQVSLKKEKAILQATLREKKLRVENAKLKEIE 60
Db 1 MATNDVAVLRLKLEQKGAADQIIEYLKQVALLKEKAILQATMREKKLRVENAKLKEIE 60
Qy 61 ELKQELIQAETQNGVKQIAPPSTGPLHANSVMSENVIQSTAV-TTVSSGTYKEQIKGTTGD 119
Db 61 ELKQELIAEHNGVEQVRVRLSTPLQTNCTASVSVQSPVATTASPAKQIK--AGE 118

Qy 120 EKKAKEKIEKKGEKKQKQSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYYEEV 179
 Db 119 EKKVKETKKEKKE-KQKSAASTDSKPIDASRLDLRIGCIITAKKHPDADSLYYEEV 177
 Qy 180 DVGEIAPRTVSGLVNHPLEQONRMVILLCNLKPAKMRGVLQAMVMCASSPEKIEIL 239
 Db 178 DVGEAAPRTVSGLVNHPLEQONRMVILLCNLKPAKMRGVLQAMVMCASSPEKVEIL 237
 Qy 240 APPNGSVPGDRITFDAPGEPDKELNPKKIIWEQIQPDLHTNDECVATYKGVPEVKKG 299
 Db 238 APPNGSVPGDRITFDAPGEPDKELNPKKIIWEQIQPDLHTNDECVATYKGVPEVKKG 297
 Qy 300 VCRAQTMNSGK 312
 Db 298 VCRAQTMNSGK 310

RESULT 8
 US-08-360-821B-35
 ; Sequence 35, Application US/08360821B
 ; Patent No. 6228837
 ; GENERAL INFORMATION:
 ; APPLICANT: Stern, David M.
 ; APPLICANT: Clauss, Matthias
 ; APPLICANT: Kao, Janet
 ; APPLICANT: Kayton, Mark
 ; APPLICANT: Libutti, Steven K
 ; TITLE OF INVENTION: Endothelial Monocyte Activating
 ; TITLE OF INVENTION: Polypeptide II: A Mediator Which Activates Host Response
 ; NUMBER OF SEQUENCES: 42
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooper & Dunham, LLP
 ; STREET: 1185 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.30, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/360,821B
 ; FILING DATE: 08-OCT-96
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White, John P.
 ; REGISTRATION NUMBER: 28,678
 ; REFERENCE/DOCKET NUMBER: 41735-A-PCT-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-278-0400
 ; TELEFAX: 212-391-0525
 ; INFORMATION FOR SEQ ID NO: 35:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 310 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-360-821B-35

Query Match 85.4%; Score 1343; DB 3; Length 310;
 Best Local Similarity 85.9%; Pred. No. 1.5e-115;
 Matches 269; Conservative 13; Mismatches 27; Indels 4; Gaps 3;
 Qy 1 MANNDVLRLEQKGAEDQIIEYKQVSLKKEKAILQATLREKKLRVENAKLKXIE 60
 Db 1 MATNDVLRLEQKGAEDQIIEYKQVSLKKEKAILQATLREKKLRVENAKLKXIE 60
 Qy 61 ELKQELIQAEIONGVKQAFPSGTPHANSVMVSENVIQSTAV-TTVSGTKEQIKGGTGD 119
 Db 61 ELKQELILAEIHNGVEQVRVRLSTPLQTNCTASESVQSPSVATTASPATKEQIK--AGE 118

Qy 120 EKKAKEKIEKKGEKKQKQSIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYYEEV 179
 Db 119 EKKVKETKKEKKE-KQKSAASTDSKPIDASRLDLRIGCIITAKKHPDADSLYYEEV 177
 Qy 180 DVGEIAPRTVSGLVNHPLEQONRMVILLCNLKPAKMRGVLQAMVMCASSPEKIEIL 239
 Db 178 DVGEAAPRTVSGLVNHPLEQONRMVILLCNLKPAKMRGVLQAMVMCASSPEKVEIL 237
 Qy 240 APPNGSVPGDRITFDAPGEPDKELNPKKIIWEQIQPDLHTNDECVATYKGVPEVKKG 299
 Db 238 APPNGSVPGDRITFDAPGEPDKELNPKKIIWEQIQPDLHTNDECVATYKGVPEVKKG 297
 Qy 300 VCRAQTMNSGK 312
 Db 298 VCRAQTMNSGK 310

RESULT 9
 US-09-851-026-35
 ; Sequence 35, Application US/09851026
 ; Patent No. 6734168
 ; GENERAL INFORMATION:
 ; APPLICANT: Stern, David M.
 ; APPLICANT: Clauss, Matthias
 ; APPLICANT: Kao, Janet
 ; APPLICANT: Kayton, Mark
 ; APPLICANT: Libutti, Steven K
 ; TITLE OF INVENTION: Endothelial Monocyte Activating
 ; TITLE OF INVENTION: Polypeptide II: A Mediator Which Activates Host Response
 ; NUMBER OF SEQUENCES: 42
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooper & Dunham, LLP
 ; STREET: 1185 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.30, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/851,026
 ; FILING DATE: 07-May-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/360,821
 ; FILING DATE: 08-OCT-96
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White, John P.
 ; REGISTRATION NUMBER: 28,678
 ; REFERENCE/DOCKET NUMBER: 41735-A-PCT-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-278-0400
 ; TELEFAX: 212-391-0525
 ; INFORMATION FOR SEQ ID NO: 35:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 310 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 35:
 ; US-09-851-026-35

Query Match 85.4%; Score 1343; DB 4; Length 310;
 Best Local Similarity 85.9%; Pred. No. 1.5e-115;
 Matches 269; Conservative 13; Mismatches 27; Indels 4; Gaps 3;
 Qy 1 MANNDVLRLEQKGAEDQIIEYKQVSLKKEKAILQATLREKKLRVENAKLKXIE 60
 Db 1 MATNDVLRLEQKGAEDQIIEYKQVSLKKEKAILQATLREKKLRVENAKLKXIE 60

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2005, 21:51:44 ; Search time 159 Seconds
(without alignments)
764.514 Million cell updates/sec

Title: US-10-623-567A-1

Perfect score: 1573

Sequence: 1 MANNDVAVLKRLKQGAADQ.....FEVKGKVCRAQTMSNSGIK 312

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1745140 seqs, 38960808 residues

Total number of hits satisfying chosen parameters: 1745140

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:*
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1573	100.0	312	17 US-10-494-940-47	Sequence 47, Appl
2	1573	100.0	312	17 US-10-623-567A-1	Sequence 1, Appl
3	1568	99.7	312	9 US-09-851-026-36	Sequence 36, Appl
4	1343	85.4	310	9 US-09-851-026-35	Sequence 35, Appl
5	951	60.5	183	17 US-10-910-403-7	Sequence 7, Appl
6	835	53.1	166	9 US-09-851-026-11	Sequence 11, Appl
7	831	52.8	166	10 US-09-930-169-3	Sequence 3, Appl
8	831	52.8	166	16 US-10-823-730-3	Sequence 3, Appl
9	709	45.1	147	10 US-09-930-169-1	Sequence 1, Appl
10	709	45.1	147	16 US-10-823-730-1	Sequence 1, Appl
11	528	33.6	353	15 US-10-424-599-180396	Sequence 180396,

12	517.5	32.9	377	16	US-10-425-115-350232	Sequence 350232,
13	517	32.9	804	16	US-10-437-963-183001	Sequence 183001,
14	516	32.8	108	10	US-09-930-169-2	Sequence 2, Appl
15	516	32.8	108	16	US-10-823-730-2	Sequence 2, Appl
16	511	32.5	792	16	US-10-437-963-183003	Sequence 183003,
17	510.5	32.5	810	15	US-10-425-114-37579	Sequence 37579, A
18	506.5	32.2	802	16	US-10-425-115-350231	Sequence 350231, A
19	497.5	31.6	192	16	US-10-767-701-36700	Sequence 36700, A
20	451	28.7	536	9	US-09-813-718-2	Sequence 2, Appl
21	451	28.7	536	15	US-10-240-532-2	Sequence 2, Appl
22	451	28.7	536	16	US-10-240-527A-2	Sequence 2, Appl
23	450	28.6	528	16	US-10-370-715B-372	Sequence 372, Appl
24	440.5	28.0	301	10	US-09-919-039-132	Sequence 132, App
25	430.5	27.4	178	9	US-09-813-718-6	Sequence 6, Appl
26	430.5	27.4	178	15	US-10-240-532-6	Sequence 6, Appl
27	430.5	27.4	178	16	US-10-240-527A-6	Sequence 6, Appl
28	429.5	27.3	168	17	US-10-910-403-2	Sequence 2, Appl
29	412	26.2	299	15	US-10-424-599-157861	Sequence 157861,
30	407.5	25.9	423	16	US-10-767-701-44089	Sequence 44089, A
31	402	25.6	409	16	US-10-437-963-109255	Sequence 109255,
32	389.5	24.8	351	16	US-10-425-115-197042	Sequence 197042,
33	378	24.0	267	15	US-10-425-114-53595	Sequence 53595, A
34	378	24.0	267	16	US-10-425-115-327897	Sequence 327897,
35	370.5	23.6	141	16	US-10-425-115-361131	Sequence 361131,
36	369.	23.5	256	15	US-10-424-599-240858	Sequence 240858,
37	366	23.3	254	16	US-10-767-701-41506	Sequence 41506, A
38	337.5	21.5	185	16	US-10-437-963-163246	Sequence 163246,
39	315.5	20.1	217	16	US-10-425-115-283649	Sequence 283649,
40	293	18.6	58	9	US-09-813-718-22	Sequence 22, Appl
41	293	18.6	58	15	US-10-240-532-22	Sequence 22, Appl
42	293	18.6	58	16	US-10-240-527A-22	Sequence 22, Appl
43	291.5	18.5	364	16	US-10-425-115-304067	Sequence 304067,
44	253	16.1	158	16	US-10-425-115-197045	Sequence 197045,
45	233	14.8	307	15	US-10-424-599-157860	Sequence 157860,

ALIGNMENTS

RESULT 1
US-10-494-940-47
; Sequence 47, Application US/10494940
; Publication No. US20050069886A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies, Inc
; TITLE OF INVENTION: REGULATED PROSTATE CANCER GENES
; FILE REFERENCE: OGT 9U 803 PCT
; CURRENT APPLICATION NUMBER: US/10/494,940
; CURRENT FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: 60/331,042
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/331,041
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/340,251
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 60/344,791
; PRIOR FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 47
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-494-940-47

Query Match 100.0%; Score 1573; DB 17; Length 312;
Best Local Similarity 100.0%; Pred. No. 1.2e-118;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MANNDVAVLKRLKQGAADQIIEYVKQVSLKKEAIQATLREKKLRVENAKLKKKIE 60
Db 1 MANNDVAVLKRLKQGAADQIIEYVKQVSLKKEAIQATLREKKLRVENAKLKKKIE 60

Qy 61 ELKQELIQAIQNGVKQIAPPSTGPLHANSVSENVISTAVTTVSSGTKEQIKGGTGDE 120
Db |||||
Qy 61 ELKQELIQAIQNGVKQIAPPSTGPLHANSVSENVISTAVTTVSSGTKEQIKGGTGDE 120
Db |||||
Qy 121 KKAKEKIEKKGEKKKQSQIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEVD 180
Db |||||
Qy 121 KKAKEKIEKKGEKKKQSQIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEVD 180
Db |||||
Qy 181 VGEIAPRTVTVSGLVNHVPLEQMNRMVILLCNLKPQKRGVLSQAMVWCASSPEKIEILA 240
Db |||||
Qy 181 VGEIAPRTVTVSGLVNHVPLEQMNRMVILLCNLKPQKRGVLSQAMVWCASSPEKIEILA 240
Db |||||
Qy 241 PPNQSVPGDRITTFDAFPGEPPDKELNPKKTIWEQIQPDLHTNDECVATYKGVPEVKGKV 300
Db |||||
Qy 241 PPNQSVPGDRITTFDAFPGEPPDKELNPKKTIWEQIQPDLHTNDECVATYKGVPEVKGKV 300
Db |||||
Qy 301 CRAFTMSNSGIK 312
Db |||||
Qy 301 CRAFTMSNSGIK 312
Db |||||

RESULT 2

US-10-623-567A-1
; Sequence 1, Application US/10623567A
; Publication No. US20050119175A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Sunghoon
; TITLE OF INVENTION: Method for Stimulating Wound Healing
; FILE REFERENCE: 012679-093
; CURRENT APPLICATION NUMBER: US/10/623,567A
; CURRENT FILING DATE: 2003-07-22
; PRIOR APPLICATION NUMBER: KR 10-2002-42858
; PRIOR FILING DATE: 2002-07-22
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-623-567A-1

Query Match 100.0%; Score 1573; DB 17; Length 312;
Best Local Similarity 100.0%; Pred. No. 1.2e-118;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MANNDVLRLEQKGAADQII EYLVKQVSLKKEKAILQATLREKKLRVENAKLKEIE 60
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Qy 61 ELKQELIQAIQNGVKQIAPPSTGPLHANSVSENVISTAVTTVSSGTKEQIKGGTGDE 120
Db |||||
Qy 61 ELKQELIQAIQNGVKQIAPPSTGPLHANSVSENVISTAVTTVSSGTKEQIKGGTGDE 120
Db |||||
Qy 121 KKAKEKIEKKGEKKKQSQIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEVD 180
Db |||||
Qy 121 KKAKEKIEKKGEKKKQSQIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEVD 180
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Qy 181 VGEIAPRTVTVSGLVNHVPLEQMNRMVILLCNLKPQKRGVLSQAMVWCASSPEKIEILA 240
Db |||||
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Qy 241 PPNQSVPGDRITTFDAFPGEPPDKELNPKKTIWEQIQPDLHTNDECVATYKGVPEVKGKV 300
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RESULT 3
US-09-851-026-36
; Sequence 36, Application US/09851026

; Patent No. US20020160957A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; Clauss, Matthias
; Kao, Janet
; Kayton, Mark
; Libutti, Steven K
; TITLE OF INVENTION: Endothelial Monocyte Activating
; Polypeptide II: A Mediator Which Activates Host Response
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Cooper & Dunham, LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.30, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/851,026
; FILING DATE: 07-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,821
; FILING DATE: 08-OCT-96
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41735-A-PCT-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 312 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-851-026-36

Query Match 99.7%; Score 1568; DB 9; Length 312;
Best Local Similarity 99.7%; Pred. No. 3e-118;
Matches 311; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 121 KKAKEKIEKKGEKKKQSQIAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEVD 180
Db |||||
Qy 181 VGEIAPRTVTVSGLVNHVPLEQMNRMVILLCNLKPQKRGVLSQAMVWCASSPEKIEILA 240
Db |||||
Qy 181 VGEIAPRTVTVSGLVNHVPLEQMNRMVILLCNLKPQKRGVLSQAMVWCASSPEKIEILA 240
Db |||||
Qy 241 PPNQSVPGDRITTFDAFPGEPPDKELNPKKTIWEQIQPDLHTNDECVATYKGVPEVKGKV 300
Db |||||
Qy 241 PPNQSVPGDRITTFDAFPGEPPDKELNPKKTIWEQIQPDLHTNDECVATYKGVPEVKGKV 300
Db |||||
Qy 301 CRAFTMSNSGIK 312
Db |||||
Qy 301 CRAFTMSNSGIK 312
Db |||||

```

Db      238 APNGSVPGDRIITFDAPGEPDKELNPKKKIWEIQIPDLHTNAECVATYKGAPFEVKGGK 299
Qy      300 VCRAQTMSNGIK 312
        |||||:||||
Db      298 VCRAQTMSNGIK 310

RESULT 5
US-10-910-403-7
; Sequence 7, Application US/10910403
; Publication No. US20050048616A1
; GENERAL INFORMATION:
; APPLICANT: Coleman et al.
; TITLE OF INVENTION: Endothelial Monocyte Activating Polypeptide III
; FILE REFERENCE: PF20601
; CURRENT APPLICATION NUMBER: US/10/910,403
; CURRENT FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: US/08/972,301
; PRIOR FILING DATE: 1997-11-18
; PRIOR APPLICATION NUMBER: US 08/483,534
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-910-403-7

Query Match          60.5%; Score 951; DB 17; Length 183;
Best Local Similarity 100.0%; Pred. No. 9.9e-69;
Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy      130 KGEKKEKKQQSIAGSADSKPIDVSRLLRLIGCIITARKHPDADSLYVEVDVGEIAPRTV 1899
        |||||:|||||
Db      1   KGEKKEKKQQSIAGSADSKPIDVSRLLRLIGCIITARKHPDADSLYVEVDVGEIAPRTV 60

Qy      190 VSGLVNHVPLEQMQRNVILLCNLKPAKRGVLISQAMWCASSPEKIEILAPPNGSVPGD 2499
        |||||:|||||
Db      61  VSGLVNHVPLEQMQRNVILLCNLKPAKRGVLISQAMWCASSPEKIEILAPPNGSVPGD 1200

Qy      250 RITFDAPGEPDKELNPKKKIWEIQIPDLHTNDEC VATYKGVFPFVKGGVCRAQTMSNS 3099
        |||||:|||||
Db      121 RITFDAPGEPDKELNPKKKIWEIQIPDLHTNDEC VATYKGVFPFVKGGVCRAQTMSNS 1800

Qy      310 GIK 312
        ||||
Db      181 GIK 183

RESULT 6
US-09-851-026-11
; Sequence 11, Application US/09851026
; Patent No. US20020160957A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
;           Clausen, Matthias
;           Kao, Janet
;           Kayton, Mark
;           Libutti, Steven K
; TITLE OF INVENTION: Endothelial Monocyte Activating
;                   Polypeptide II: A Mediator Which Activates Host
;                   NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham, LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.30, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/851,026
FILING DATE: 07-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/360,821
FILING DATE: 08-OCT-96
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41735-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-851-026-11

Query Match 53.1%; Score 835; DB 9; Length 166;
Best Local Similarity 94.0%; Pred. No. 2e-59;
Matches 156; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
QY 147 SKPIDVSRDLRIGCIITARKHPDADSLYYVEVDVGEIAPRTVTVSGLVNHHVPLEQMQRN 206
DB 1 SKPIDARLRLRIGCIITAKKHPDADSLYYVEVDVGEAPRTVTVSGLVNHHVPLEQMQRN 60
QY 207 VILLCNLKPAMRGVLSQAMVMCASSPEKIEILAPPNGSVPGDRITTFDAPFGDPKELNP 266
DB 61 VVLLCNLKPAMRGVLSQAMVMCASSPDKVEILAPPNGSVPGDRITTFDAPFGDPKELNP 120
QY 267 KKKIWEQIQPDLNTHNDECVAITYKVPFEVKGKVCRAQTWNSGIK 312
DB 121 KKKIWEQIQPDLNTHNDECVAITYKGPAPFEVKGKVCRAQTWNSGIK 166

RESULT 7
US-09-930-169-3
Sequence 3, Application US/09930169
Publication No. US20030004309A1
GENERAL INFORMATION:
APPLICANT: KIM, SUNGHOON
APPLICANT: KO, YOUNG-GYU
TITLE OF INVENTION: IMMUNOLOGICAL ENHANCEMENT AGENT COMPRISING N-TERMINAL PEPTIDE OF
FILE REFERENCE: 058333/0106
CURRENT APPLICATION NUMBER: US/09/930,169
CURRENT FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: KR 2001-31310
PRIOR FILING DATE: 2001-06-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 166
TYPE: PRT
ORGANISM: Unknown Organism
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: Mammalian
OTHER INFORMATION: protein sequence
US-09-930-169-3

Query Match 52.8%; Score 831; DB 10; Length 166;
Best Local Similarity 100.0%; Pred. No. 4.3e-59;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 91 MVSENVISQAVTTVSSGTKEQIKGGTGDEKKAKEIEKKGEKKQKQSIAGSADSKPI 150

DB 1 MVSENVISQAVTTVSSGTKEQIKGGTGDEKKAKEIEKKGEKKQKQSIAGSADSKPI 60
QY 151 DVSRDLRIGCIITARKHPDADSLYYVEVDVGEIAPRTVTVSGLVNHHVPLEQMQRN 210
DB 61 DVSRDLRIGCIITARKHPDADSLYYVEVDVGEIAPRTVTVSGLVNHHVPLEQMQRN 120
QY 211 CNLKPAMRGVLSQAMVMCASSPEKIEILAPPNGSVPGDRITTFDAF 256
DB 121 CNLKPAMRGVLSQAMVMCASSPEKIEILAPPNGSVPGDRITTFDAF 166

RESULT 8
US-10-823-730-3
Sequence 3, Application US/10823730
Publication No. US20040185060A1
GENERAL INFORMATION:
APPLICANT: IMAGENE CO., LTD.
TITLE OF INVENTION: Immunological enhancement agent comprising N-terminal peptide of
FILE REFERENCE: NPF1918
CURRENT APPLICATION NUMBER: US/10/823,730
CURRENT FILING DATE: 2004-04-14
NUMBER OF SEQ ID NOS: 11
SOFTWARE: KopatentIn 1.71
SEQ ID NO 3
LENGTH: 166
TYPE: PRT
ORGANISM: mammalian
US-10-823-730-3

Query Match 52.8%; Score 831; DB 16; Length 166;
Best Local Similarity 100.0%; Pred. No. 4.3e-59;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 91 MVSENVISQAVTTVSSGTKEQIKGGTGDEKKAKEIEKKGEKKQKQSIAGSADSKPI 150
DB 1 MVSENVISQAVTTVSSGTKEQIKGGTGDEKKAKEIEKKGEKKQKQSIAGSADSKPI 60
QY 151 DVSRDLRIGCIITARKHPDADSLYYVEVDVGEIAPRTVTVSGLVNHHVPLEQMQRN 210
DB 61 DVSRDLRIGCIITARKHPDADSLYYVEVDVGEIAPRTVTVSGLVNHHVPLEQMQRN 120
QY 211 CNLKPAMRGVLSQAMVMCASSPEKIEILAPPNGSVPGDRITTFDAF 256
DB 121 CNLKPAMRGVLSQAMVMCASSPEKIEILAPPNGSVPGDRITTFDAF 166

RESULT 9
US-09-930-169-1
Sequence 1, Application US/09930169
Publication No. US20030004309A1
GENERAL INFORMATION:
APPLICANT: KIM, SUNGHOON
APPLICANT: KO, YOUNG-GYU
TITLE OF INVENTION: IMMUNOLOGICAL ENHANCEMENT AGENT COMPRISING N-TERMINAL PEPTIDE OF
FILE REFERENCE: 058333/0106
CURRENT APPLICATION NUMBER: US/09/930,169
CURRENT FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: KR 2001-31310
PRIOR FILING DATE: 2001-06-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 147
TYPE: PRT
ORGANISM: Unknown Organism
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: Mammalian
OTHER INFORMATION: protein sequence
US-09-930-169-1

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; OTHER INFORMATION: Clone ID: PAT_MRT3847_13392C.1.1.pap
US-10-424-599-180396

Query Match      33.6%; Score 528; DB 15; Length 353;
Best Local Similarity 43.6%; Pred. No. 3.5e-34;
Matches 113; Conservative 41; Mismatches 79; Indels 26; Gaps 4;

Qy      56 KKEIEELKOEILQAEIQNGVKQIAFPSTGTPHLANSMVSENVIQSTAVTTVSSGTKEQIKG 115
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      119 KPLFRELKDE-----EVEFVRKFPAGSQADRIVPRAEAEQNVARQLKTKYVSDGNGKKKPG 174
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy      116 GTGDEKFAKEIKETKGEKKEKQOQSIAGSADSKPIDVSRDLRLRIGICITARKHPDADSLY 175
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      175 KSSNEAKNK-----AAAPEDITITRLDIRVGLIIRKQKHPDADALY 215

Qy      176 VERVDVGETAPRTVWSGLNVHVPLEOMQRNWLILCNLPKAKRGVLSQAMVWCASSPE- 234
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      216 VEEIDVGESEQTRTVWSGLVKFIFLDEMQRNKKVCLCNLPVTVWRGKTSQAMVLAASGDGH 275

Qy      235 -KTEILAPPNGSPVPGDRITFDAPPGPDKEINPKKIWEQIQDLDHTNDECVATYKGVPF 293
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      276 TKVELVEPPSSAQPGRIITFPFGVEGNPDELLNPKKVKWETLQVLDLHTNEELVACYKNVPL 335

Qy      294 EVKKGVCVCAQTMSNGIK 312
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db      336 TTSA-GVCKYSSISCGSIR 353
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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216 VEEIDVGEETRVTVSGLVKFIPLDEMQRKVCVLNCLKPVTTMRGIKSQAMVLAASGDGH 275
Qy 235 -KTEILLAPNGSVPGDRITFDAPPGEPDKELANPKKIWEQIOPLDHTNDESCVATYKGVPF 293
Db 276 TKVELVEPPSSAQGGRITFPGTEGNPDELLNPKKWETLQVLDLHTNEELVACYKVVPL 335
Qy 294 EVKKGVCVCAQTMSNSGIX 312
Db 336 TTSAGVCKVSSISCGSIR 353

RESULT 12
US-10-425-115-350232
; Sequence 350232, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.

```

```

; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated wi
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 350232
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(377)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_82583C.1.pep
; US-10-425-115-350232

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US-10-425-115-350232	Query Match	32.9%;	Score 517.5;	DB 16;	Length 377;
	Best Local Similarity	38.2%;	Pred. No. 2.7e-33;		
	Matches	122;	Conservative 50;	Mismatches 84;	Indels 63; Gaps 11;
Qy	18	ADQIIIEVLKQOVSILLKEKATLQATLREKKLRYENAKLKKE-----IEE 61			
Db	98	SDEVL-----ROLNLSPEENI-----SLSEKG-----EIAKAKSPWDFVPAGHRIGKPAFLPKE 147			
Qy	62	LKQELIQAEIQNGVKQIAPPSPGTPHANSVMSENVIOSTAVTTVSSGCK--EQIKGGTGD 119			
Db	148	LKDE-----DVALHEKTAGSQAESKCAADAANKVANQLKG--- 186			
Qy	120	EKKAKEIKIEKGEKKKQOOSIAGSADSKPID----VSRLDLRGTGCIITARKHPDADSLY 175			
Db	187	-----TKLSDRGTGKEPKQOS--GGSKSTADADITVAKLDIRVGLIRKAEKHPDADSLY 239			
Qy	176	VEEVVDVGEIAPRTVTVSGLVNHPLEQONRWVILLCNLKKAKRGCVLSQAMWCASSPE- 234			

Db 240 VEEDVGDTPRTVVSLGVKFIPLLEEMQNRKVCVLCNLKPVAMRGKSHAMVLAASNEHD 299
Qy 235 -KIEILAPPNGSVPGDRITFDAPGEPDKELNPKKTIWEQIQDPLHTNDECVATYKGVPP 293
Db 300 TKVELVPPESAAYGERVTFAGYSGEPEASLGSGSKTKWEKLAELHSGELVACVYKDVPP 359
Qy 294 EVKGGVCRAQTMSNGIK 312
Db 360 TTSA-GICKVKTIANGAIR 377

RESULT 13
US-10-437-963-183001
; Sequence 183001, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 183001
; LENGTH: 804
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_80132C.1.pap
US-10-437-963-183001

Query Match 32.9%; Score 517; DB 16; Length 804;
Best Local Similarity 38.1%; Pred. No. 8.4e-33;
Matches 117; Conservative 53; Mismatches 79; Indels 58; Gaps 9;
Qy 35 KAILOATLREBKLI-----RVENAKLKE-----IELKQELIOAEIQN 73
Db 527 EVLLQLNMTPEESLSFCDCKGEIAKARPWDFVSAGHKIGKPSPLFKELDKEVES---- 582
Qy 74 GVKQIAPFSGTPLHANSMVSENVIQSTAVTTVSSGK--BQIKGGTGDEKKAKEIKKKG 131
Db 583 -----FRNKFAGSQAERSKQAQADAEAKKVADKLKG-----TKLSDGG 620
Qy 132 EKKEKKQOSIAGSDSK-----PIDVSRDLRLRIGCIITARKHPDADSLYVEVDVGEIAPR 187
Db 621 QKKEQKQS--GGSKSNAEVDVTVAKLDIRVGLIRKAQHPDADSLYVEIDVGEAPR 678
Qy 188 TVSGLVNHVPLEQMQNRWVLLCNLKPAMRGVLSQAMVNCASSPS--KIEILAPPNGS 245
Db 679 TVVSLGVKFIPLLEEMQNRKVCVLCNLKPVAMRGKSHAMVLAASNEHDKVELVEPPESA 738
Qy 246 VPGDRITFDAPGEPDKELNPKKTIWEQIQDPLHTNDECVATYKGVPPFEVKGKVCRAQT 305
Db 739 AVGERVTFAGYSGEPEASLNAKSTWEKLSADLHSGELVACVYKDVPPFTTSA-GVCKVKS 797
Qy 306 MNSGK 312
Db 798 IASGEIR 804

RESULT 14
US-09-930-169-2
; Sequence 2, Application US/09930169
; Publication No. US20030004309A1
; GENERAL INFORMATION:
; APPLICANT: KIM, SUNGHOON

; APPLICANT: KO, YOUNG-GYU
; TITLE OF INVENTION: IMMUNOLOGICAL ENHANCEMENT AGENT COMPRISING N-TERMINAL PEPTIDE OF
; FILE REFERENCE: P43 AS AN EFFECTIVE COMPONENT
; CURRENT APPLICATION NUMBER: US/09/930,169
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: KR 2001-31310
; PRIOR FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Mammalian
; OTHER INFORMATION: protein sequence
US-09-930-169-2

Query Match 32.8%; Score 516; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 6.5e-34;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MANNDVAVLKELEQKGAEADQIIEYLKQOVSLKKEKAILQATLREKKLRVENAKLKEIE 60
Db 1 MANNDVAVLKELEQKGAEADQIIEYLKQOVSLKKEKAILQATLREKKLRVENAKLKEIE 60
Qy 61 ELKQELIOAEIQNGVKQIAPFSGTPLHANSMVSENVIQSTAVTTVSSG 108
Db 61 ELKQELIOAEIQNGVKQIAPFSGTPLHANSMVSENVIQSTAVTTVSSG 108

RESULT 15
US-10-823-730-2
; Sequence 2, Application US/10823730
; Publication No. US20040185060A1
; GENERAL INFORMATION:
; APPLICANT: IMAGENE CO., LTD.
; TITLE OF INVENTION: Immunological enhancement agent comprising N-terminal peptide of
; FILE REFERENCE: NPF1918
; CURRENT APPLICATION NUMBER: US/10/823,730
; CURRENT FILING DATE: 2004-04-14
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 2
; LENGTH: 108
; TYPE: PRT
; ORGANISM: mammalian
US-10-823-730-2

Query Match 32.8%; Score 516; DB 16; Length 108;
Best Local Similarity 100.0%; Pred. No. 6.5e-34;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MANNDVAVLKELEQKGAEADQIIEYLKQOVSLKKEKAILQATLREKKLRVENAKLKEIE 60
Db 1 MANNDVAVLKELEQKGAEADQIIEYLKQOVSLKKEKAILQATLREKKLRVENAKLKEIE 60
Qy 61 ELKQELIOAEIQNGVKQIAPFSGTPLHANSMVSENVIQSTAVTTVSSG 108
Db 61 ELKQELIOAEIQNGVKQIAPFSGTPLHANSMVSENVIQSTAVTTVSSG 108

Search completed: August 3, 2005, 22:01:39
Job time : 161 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2005, 21:45:34 ; Search time 174 Seconds
(without alignments)

918.211 Million cell updates/sec

Title: US-10-623-567A-1

Perfect score: 1573

Sequence: 1 MANNDVLRKLEQKGAEDQ.....FEVKGKGVCAQTMSNSGIK 312

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1573	100.0	312	1	MCAL_HUMAN
2	1362.5	86.6	359	1	MCAL_CRIGR
3	1343	85.4	310	1	MCAL_MOUSE
4	1338	85.1	319	2	Q8C2U7
5	1084	68.9	297	2	Q7ZWM7
6	671	42.7	323	2	Q9V504
7	625.5	39.8	351	2	Q7Q8S7
8	564	35.9	917	1	SYM_CABEL
9	517	32.9	804	1	SYM_ORISA
10	499.5	31.8	149	2	Q62542
11	499	31.7	797	1	SYM_ATH
12	453.5	28.8	529	2	Q6TGS6
13	451.5	28.7	529	2	Q6DF27
14	450	28.6	527	1	SYM_BOVIN
15	450	28.6	527	1	SYM_HUMAN
16	446.5	28.4	527	1	SYM_MOUSE
17	441.5	28.1	373	2	Q6BY38
18	441.5	28.1	450	2	Q9P6K7
19	440	28.0	528	2	Q7ZX51
20	439	27.9	528	2	Q6D1U1
21	429	27.3	376	1	G4P1_YEAST
22	426	27.1	376	2	Q6FNNO
23	423.5	26.9	371	2	Q754V3
24	415	26.4	372	2	Q6CK16
25	402	25.6	409	2	Q8RUP8
26	401.5	25.5	394	2	Q6C763
27	400.5	25.5	389	2	Q93VB0
28	400.5	25.5	440	2	Q7XJW9
29	395	25.1	525	2	Q9VV60
30	391	24.9	252	2	Q7XVQ8
31	388	24.7	78	2	Q9EPV3

RESULT 1

MCAL_HUMAN STANDARD; PRT; 312 AA.

AC Q12904; Q96CQ9;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Multisynthetase complex auxiliary component p43 [Contains:

DE Endothelial-monocyte activating polypeptide II (EMAP-II) (Small

DE Inducible cytokine subfamily E member 1)]

GN Name=SCYB1; Synonyms=EMAP2;

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RP MEDLINE=95014290; PubMed=7929199;

RA Kao J., Houck K., Fan Y., Haehnel I., Libutti S.K., Kayton M.L.,

RA Grikscheit T., Chabot J., Nowyrod R., Greenberg S., Kuang W.J.,

RA Leung D.W., Hayward J.R., Kiesel W., Heath M., Brett J., Stern D.M.;

RT "Characterization of a novel tumor-derived cytokine. Endothelial-

RL J. Biol. Chem. 269:25106-25119(1994).

RN [2]

RP SEQUENCE FROM N.A.

RP TISSUE=Pancreas;

RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S., Kravinsky M.I., Skalska U., Smallos D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RL and mouse cDNA sequences."

CC -1- SIMILARITY: Contains 1 tRNA-binding domain.

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EMBL; U01117; AAA62202.1; --
DR EMBL; BC014051; AAI14051.1; --
DR PDB; 1E72; X-ray; A=147-312.
DR PDB; 1EUJ; X-ray; A/B=147-312.
DR PDB; 1FLO; X-ray; A=150-312.
DR Genew; HGNC:10648; SCY1.
DR H-invDB; HIX0004426; --
DR MIM; 603605; --
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005125; F:cytokine activity; TAS.
DR GO; GO:0000049; F:RNA binding; TAS.
DR GO; GO:0006935; P:chemotaxis; TAS.
DR GO; GO:0006954; P:inflammatory response; TAS.
DR GO; GO:0006418; P:RNA aminoacylation for protein translation; TAS.
DR InterPro; IPR008232; EMAP11.
DR InterPro; IPR008994; Nucleic acid OB.
DR Pfam; PF01588; tRNA_bind; 1.
DR PIRSF; PIRSF005381; EMAP11; 1.
DR PROSITE; PS00886; TRBD; 1.
DR 3D-structure; Cytokine; Protein biosynthesis; RNA-binding;
trNA-binding.
FT PROPEP 1 146
FT CHAIN 147 312
FT DOMAIN 151 252
FT CONFLICT 79 79
FT HELIX 152 154
FT STRAND 157 168
FT TURN 169 170
FT STRAND 171 180
FT STRAND 187 191
FT TURN 194 196
FT HELIX 199 202
FT TURN 203 204
FT STRAND 205 210
FT STRAND 216 217
FT STRAND 222 223
FT STRAND 226 227
FT STRAND 229 232
FT TURN 233 234
FT STRAND 235 238
FT STRAND 240 240
FT TURN 243 244
FT TURN 247 248
FT STRAND 250 250
FT STRAND 254 255
FT TURN 266 268
FT TURN 270 270
FT TURN 271 274
FT HELIX 275 277
FT STRAND 278 280
FT TURN 282 283
FT STRAND 285 288
FT TURN 289 290
FT STRAND 291 292
FT STRAND 294 295
FT TURN 296 298
FT STRAND 299 300
FT STRAND 302 302
FT STRAND 310 312
SQ SEQUENCE 312 AA; 34326 MW; 946310A0216F7587 CRC64;
Query Match 100.0%; Score 1573; DB 1; Length 312;
Best Local Similarity 100.0%; Pred. No. 4e-83;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MANNDVAVLRLEQKGABADQIIEYLKQVSLLEKKAIIQATLREKKLRVENAKLKEIE 60
|||||

Db 1 MANNDVAVLRLEQKGABADQIIEYLKQVSLLEKKAIIQATLREKKLRVENAKLKEIE 60
QY 61 ELKQELIQAEIQNGVKQIAFPSPGTPHANSWSENVIQSTAVTTVSSGTEKQIKGGTGDE 120
|||
Db 61 ELKQELIQAEIQNGVKQIAFPSPGTPHANSWSENVIQSTAVTTVSSGTEKQIKGGTGDE 120
|||
QY 121 KKAKEIEKKGEKKEKQKQSIAGSADSKPIDVSRDLRLTGCIITARKHPDADSLYVEVD 180
|||
Db 121 KKAKEIEKKGEKKEKQKQSIAGSADSKPIDVSRDLRLTGCIITARKHPDADSLYVEVD 180
|||
QY 181 VGEIAPRTVTVSGLVNHPLEQMONRVILLCNLKPAMRGVLSQAMVMCASSPEKIEILA 240
|||
Db 181 VGEIAPRTVTVSGLVNHPLEQMONRVILLCNLKPAMRGVLSQAMVMCASSPEKIEILA 240
|||
QY 241 PPNGSVPGDRITFDAPFGPEKDELNPKKKIWEIQIDPLHTNDECVATYKGVPEVKKGKV 300
|||
Db 241 PPNGSVPGDRITFDAPFGPEKDELNPKKKIWEIQIDPLHTNDECVATYKGVPEVKKGKV 300
|||
QY 301 CRAFTWMSNGIK 312
|||
Db 301 CRAFTWMSNGIK 312
|||
RESULT 2
MCAL CRIGR STANDARD; PRT; 359 AA.
AC Q54873;
DT 16-OCT-2001 (Rel. 40, Created)
DT 18-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Multisynthetase complex auxiliary component p43 [Contains:
DE Endothelial-monocyte activating polypeptide II (EMAP-II) (Small
DE Inducible cytokine subfamily E member 1)].
GN Name-SCY1;
OS Crictetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Crictetus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98070438; PubMed=9405472; DOI=10.1074/jbc.272.51.32573;
RA Quevillon S., Agou F., Robinson J.-C., Mirande M.;
RT "The p43 component of the mammalian multi-synthetase complex is likely
RT to be the precursor of the endothelial monocyte-activating polypeptide
RT II cytokine";
RL J. Biol. Chem. 272:32573-32579 (1997).
CC -|- SUBUNIT: Component of the multisynthetase complex which is
CC comprised of a bifunctional glutamyl-prolyl-tRNA synthetase, the
CC monospecific isoleucyl, leucyl, glutamyl, methionyl, lysyl,
CC arginyl, and aspartyl-tRNA synthetases as well as three auxiliary
CC proteins, p18, p48 and p43.
CC -|- SIMILARITY: Contains 1 tRNA-binding domain.

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CC or send an email to license@isb-sib.ch).

EMBL; AF021800; AAB95207.1; --
DR HSPSP; Q12904; 1E7Z.
DR InterPro; IPR008232; EMAP11.
DR InterPro; IPR008994; Nucleic acid OB.
DR InterPro; IPR002547; tRNA bind.
DR Pfam; PF01588; tRNA_bind; 1.
DR PIRSF; PIRSF005381; EMAP11; 1.
DR PROSITE; PS00886; TRBD; 1.
KW Cytokine; Protein biosynthesis; RNA-binding; trNA-binding.
FT PROPEP 1 194
FT CHAIN 194 359
Endothelial-monocyte activating

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FT DOMAIN 198 299 polypeptide II.
SQ SEQUENCE 359 AA; 39601 MW; 4D868D1B65D72C23 CRC64;
Query Match 86.6%; Score 1362.5; DB 1; Length 359;
Best Local Similarity 86.0%; Pred. No. 6.4e-71;
Matches 270; Conservative 19; Mismatches 22; Indels 3; Gaps 2;

QY 1 MANNDVAVLRLEQKGAADQIIIEYLKQVSLLEKEKAILQATLRREKKLRVENAKLKEIE 60
DB 47 MATNDVAVLRLEQKGAADQIIIEYLKQVALLKEKAVLQATLRREKKLRVENAKLKEIE 106
QY 61 ELKQELIAEIQNGVKQIAPP--SGTFLHANSVMSENVIQSTAVTTVSSGTEQIKGGTG 118
DB 107 ELKQELIAEIQNGVKQIPVPVQSDTPVQASSAVSTSVIQSTSVSTISCSIKHSGG-G 165
QY 119 DEKAKKIEKKGKKEKQKQSIAGSADSKPIDVSRDLRLGICITARKHPDADSLYVEE 178
DB 166 EEKVKKEKTKGKKEKQKQSAAPSADSKPVDVSRDLRLGIRIVTVKGGHPDADSLYVEE 225
QY 179 VDVGESAPRTVSGLVNHPLEQONRNVILLCNLKPQKMGVLISQAMWMCASSPEKIEI 238
DB 226 VDVGESAPRTVSGLVNHPVDQONRNVILLCNLKPQKMGVLISQAMWMCASSPEKVEI 285
QY 239 LAPNGSVPGDRITFDAPFGPEFDKELNPKKIKIWEQIQPDLTNDCEVATYKGVPEVKGK 298
DB 286 LAPNGSVPGDRITFDAPFGPEFDKELNPKKIKIWEQIQPDLTNAECVATYKGVPEVKGK 345
QY 299 GVCRAQTMSNGIK 312
DB 346 GVCRAQTMSNGIK 359

RESULT 3
MCAL MOUSE
ID MCAL MOUSE STANDARD; PRT; 310 AA.
AC P31230; Q60659;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Multisynthetase complex auxiliary component p43 [Contains:
DE Endothelial-monocyte activating polypeptide II (EMAP-II) (Small
DE inducible cytokine subfamily E member 1)].
GN Name=Scyel; Synonyms=Emap2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95014290; PubMed=7929199;
RA Kao J., Houck K., Fan Y., Haehnel I., Libutti S.K., Kayton M.L.,
RA Grikscheit T., Chabot J., Nowygrod R., Greenberg S., Kuang W.J.,
RA Leung D.W., Hayward J.R., Kiesel W., Heath M., Brett J., Stern D.M.;
RT "Characterization of a novel tumor-derived cytokine. Endothelial-
RT monocyte activating polypeptide II."
RL J. Biol. Chem. 269:25106-25119(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner B.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.A., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE OF 145-164 FROM N.A.
RX MEDLINE=93015897; PubMed=1400342;
RA Kao J., Ryan J., Brett G., Chen J., Shen H., Fan Y.-G., Godman G.,
RA Fanilietti P.C., Wang F., Pan Y.-C.E., Stern D., Clauss M.;
RT "Endothelial monocyte-activating polypeptide II: A novel tumor-derived
RT polypeptide that activates host-response mechanisms."
RL J. Biol. Chem. 267:20239-20247(1992).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=94193665; PubMed=7545917;
RA Kao J., Fan Y., Haehnel I., Brett J., Greenberg S., Clauss M., Stern D.,
RA Kayton M., Houck K., Kiesel W., Seljelid R., Burnier J., Stern D.;
RT "A peptide derived from the amino terminus of endothelial-monocyte-
RT activating polypeptide II modulates mononuclear and polymorphonuclear
RT leukocyte functions, defines an apparently novel cellular interaction
RT site, and induces an acute inflammatory response."
RL J. Biol. Chem. 269:9774-9782(1994).
CC -!- FUNCTION: Alters endothelial and monocyte functions, induces the
CC migration of monocytes and granulocytes, and induces an
CC inflammatory response in the mouse footpad model. EMAP II elicits
CC a proinflammatory response and, potentially, augments the effects of
CC the other tumor-derived cytokines.
CC -!- SUBUNIT: Monomer.
CC -!- SIMILARITY: Contains 1 tRNA-binding domain.
CC -----
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CC -----
DR EMBL; U01018; AAA62203.1; -.
DR EMBL; BC002054; AAH02054.1; -.
DR PIR; A55053; A55053.
DR HSSP; Q12904; 1EUJ.
DR MGP; MGI:102774; Scyel.
DR InterPro; IPR008232; EMAPII.
DR InterPro; IPR008994; Nucleic_acid_OB.
DR InterPro; IPR002547; tRNA_bind.
DR PIRSF; PIRSF005381; EMAPII; 1.
DR PIRSF; PIRSF005381; EMAPII; 1.
DR PROSITE; PS00886; TRBD; 1.
DR Cycokine; Protein biosynthesis; RNA-binding; tRNA-binding.
KW PROPEP 1 144
FT CHAIN 145 310 Endothelial-monocyte activating
FT polypeptide II.
FT DOMAIN 149 250 tRNA-binding.
FT SEQUENCE 310 AA; 33997 MW; A2F8FF52A33D03A0 CRC64;
Query Match 85.4%; Score 1343; DB 1; Length 310;
Best Local Similarity 85.9%; Pred. No. 7.3e-70;
Matches 269; Conservative 13; Mismatches 27; Indels 4; Gaps 3;

QY 1 MANNDVAVLRLEQKGAADQIIIEYLKQVSLLEKEKAILQATLRREKKLRVENAKLKEIE 60
DB 1 MATNDVAVLRLEQKGAADQIIIEYLKQVALLKEKAVLQATLRREKKLRVENAKLKEIE 60
QY 61 ELKQELIAEIQNGVKQIAPP--SGTFLHANSVMSENVIQSTAVTTVSSGTEQIKGGTG 119
DB 107 ELKQELIAEIQNGVKQIPVPVQSDTPVQASSAVSTSVIQSTSVSTISCSIKHSGG-G 179
QY 119 DEKAKKIEKKGKKEKQKQSIAGSADSKPIDVSRDLRLGICITARKHPDADSLYVEE 179
DB 166 EEKVKKEKTKGKKEKQKQSAAPSADSKPVDVSRDLRLGIRIVTVKGGHPDADSLYVEE 225
QY 179 VDVGESAPRTVSGLVNHPLEQONRNVILLCNLKPQKMGVLISQAMWMCASSPEKIEI 238
DB 226 VDVGESAPRTVSGLVNHPVDQONRNVILLCNLKPQKMGVLISQAMWMCASSPEKVEI 285
QY 239 LAPNGSVPGDRITFDAPFGPEFDKELNPKKIKIWEQIQPDLTNDCEVATYKGVPEVKGK 298
DB 286 LAPNGSVPGDRITFDAPFGPEFDKELNPKKIKIWEQIQPDLTNAECVATYKGVPEVKGK 345
QY 299 GVCRAQTMSNGIK 312
DB 346 GVCRAQTMSNGIK 359
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Db 119 EKKVKEKTEKGEKKE-KQSSAAASTDSKPIDASRLDLRIGCVITAKKHPDADSLYVEEV 177
Qy 180 DVGEIAPRTVTVSGLVNHPLEQONRVLLCNLKPAMRGVLSQAMVMCASSPEKIEIL 239
Db 178 DVGEIAPRTVTVSGLVNHPLEQONRVLLCNLKPAMRGVLSQAMVMCASSPEKIEIL 237
Qy 240 APPNGSVPGDRITFDAPFGPEKELNPKKKIWEIQPDLHTNDCVATYKGVPEVKKGK 299
Db 238 APPNGSVPGDRITFDAPFGPEKELNPKKKIWEIQPDLHTNAECVATYKGVPEVKKGK 297
Qy 300 VCRAQTMNSNGIK 312
Db 298 VCRAQTMNSNGIK 310

RESULT 4
ID Q8C2U7 PRELIMINARY; PRT; 319 AA.
AC Q8C2U7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-
DE length enriched library, clone:E430001B22 product:endothelial monocyte
DE activating polypeptide 2, full insert sequence.
GN Name=Scyl1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=1076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitasuna T., Tashiro H., Itoh M.,
RA Sano N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa K., Izawa M., Ohara E., Watanaki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format

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RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayaehida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Okamoto N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK087932; BAC40045.1; -.
DR HSSP; Q12904; 1EUJ.
DR MGD; MGI:102774; Scyl1.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0000049; F:RNA binding; IEA.
DR InterPro; IPR008994; Nucleic acid_OB.
DR InterPro; IPR002547; tRNA bind.
DR Pfam; PF01588; tRNA bind; 1.
DR PROSITE; PS50886; TRBD; 1.
DR PROSITE; PS50886; TRBD; 1.
SQ SEQUENCE 319 AA; 35197 MW; B977E8FE742BESC6 CRC64;

Query Match 85.1%; Score 1338; DB 2; Length 319;
Best Local Similarity 85.3%; Pred. No. 1.5e-69;
Matches 267; Conservative 15; Mismatches 27; Indels 4; Gaps 3;

Qy 1 MANDAVLKELEQGAADQIIEYLKQOYSLLEKAILQATLEEKLRVENAKLKEIE 60
Db 10 MATNDVLRLEQKGADQIIEYLKQOVALLEKAILQATMEKKLRVENAKLKEIE 69
Qy 61 ELKQELIQAEIQNGVKQIAPPSGTPHANSMVSENVISQSTAV-TTVSSSGTKQIKGTGD 119
Db 70 ELKQELILAEIHNGVEQVRVRLSTPQTCTASESVVQSPSVATTSLATKEQIK-AGE 127
Qy 120 EKKAKEIKKGEKKEKQKQSIAGSADSKPIDVSRDLDRIGCVITAKKHPDADSLYVEEV 179
Db 128 EKKVKEKTEKGEKKE-KQSSAAASTDSKPIDASRLDLRIGCVITAKKHPDADSLYVEEV 186
Qy 180 DVGEIAPRTVTVSGLVNHPLEQONRVLLCNLKPAMRGVLSQAMVMCASSPEKIEIL 239
Db 187 DVGEIAPRTVTVSGLVNHPLEQONRVLLCNLKPAMRGVLSQAMVMCASSPEKIEIL 246
Qy 240 APPNGSVPGDRITFDAPFGPEKELNPKKKIWEIQPDLHTNDCVATYKGVPEVKKGK 299
Db 247 APPNGSVPGDRITFDAPFGPEKELNPKKKIWEIQPDLHTNAECVATYKGVPEVKKGK 306
Qy 300 VCRAQTMNSNGIK 312
Db 307 VCRAQTMNSNGIK 319

RESULT 5
Q7ZWY7
ID Q7ZWY7 PRELIMINARY; PRT; 297 AA.
AC Q7ZWY7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Scyl1-prov protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;

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OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG MEDLINE=99069613; PubMed=9851916;
RX The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RL investigating biology.";
RL Science 282:2012-2018(1998).
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + tRNA(Met) = AMP +
CC di-phosphate + L-methionyl-tRNA(Met).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the class-I aminoacyl-tRNA synthetase
CC family.
CC -1- SIMILARITY: Contains 1 tRNA-binding domain.
CC -----
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CC -----
CC EMBL; Z73427; CRA97803.1; -.
CC PIR; T22898; T22898.
CC HSSP; Q12904; 1FL0.
CC WormBase; WBGene0003415; mrs-1.
CC WormPeP; P58B3.5; CE06007.
CC InterPro; IPR008224; MetRS dimerising.
CC InterPro; IPR008994; Nucleic acid OB.
CC InterPro; IPR002300; tRNA-synt_1a.
CC InterPro; IPR001412; tRNA-synt_1.
CC InterPro; IPR002304; tRNA-synt_met.
CC InterPro; IPR002547; tRNA_bind.
CC InterPro; IPR009080; tRNA-synt_1.
CC Pfam; PF00133; tRNA-synt_1.
CC Pfam; PF01588; tRNA_bind.
CC PIRSF; PIRSF001528; MetRS dimerising; 1.
CC PRINTS; PR01041; TRNASYNTHMET.
CC TIGRFAMs; TIGR00398; metG; 1.
CC PROSITE; PS00178; AA tRNA_LIGASE_I; 1.
CC Aminoacyl-tRNA synthetase; ATP-binding; Ligase; Protein biosynthesis;
CC RNA-binding; tRNA-binding.
CC SITE 44 54 "HIGH" region.
CC SITE 367 371 "KMSKS" region.
CC BINDING 370 370 ATP (By similarity).
CC DOMAIN 756 857 tRNA-binding.
CC SEQUENCE 917 AA; 101713 MW; 3B42AABA314PBDFO CRC64;

Query Match 35.9%; Score 564; DB 1; Length 917;
Best Local Similarity 42.3%; Pred. No. 2.1e-24;
Matches 135; Conservative 52; Mismatches 100; Indels 32; Gaps 8;

QY 1 MANNDVLLKRLKQKAEADQII-EYLKQVSLLEKAILQATLREKKLRVENAKLKEI 59
DB 624 NASTAAAFVE-LEQGAKVISQLIAQLKK---FDQAKALF--TRNQLQDLGDKNQLTTIDV 677
QY 60 EELKQELQAEITQNGVKQIAFP--SGTPLHANSWSENVIQSTAVTTVSSGTEKQIKGGT 117
DB 678 KTLQHQLELETAAGIKQVPEVUSCTP-----TPSTPASGLITE----- 718
QY 118 GDEKAKKEIKKGGKKEKQKQSIAGSADSKP-----IDVSRDLDRIGCIITARKHPDADS 173
DB 719 APKKEAPSTPAPSEPKAKEQKGGKGAAPVDVTIDVGRGLDMRVGRIIKEKHPDADA 778
QY 174 LYVEVDVGETAPRTVWGLNVHVPLEQONRMWILLCNLPKAKRGVLSQAMWNCASSP 233
DB 779 LYVEQIDVGESAPRTVWGLSVHVPDQNRLLVVLVVLNLPKAKRGVSRAMWNCASSP 838
QY 234 EKIEI LAPNGSVGDRITFDAPGCEPKELNPKKIWEQIQPDLTHTNDECVATYKGVFP 293

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Db 839 DKVEIMEVPADSKPGTVPVCPYTHRPDEQLNPKKIKIETWAEADLKVSASGPAENKQPL 898
QY 294 EVKKGKGVCAQATMSNGIK 312
Db 899 LIGSESKWTAPTTLRGVHVK 917

RESULT 9
ID_SYM ORYSA STANDARD; PRT; 804 AA.
AC Q9ZTS1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Probable methionyl-tRNA synthetase (EC 6.1.1.10) (Methionine--tRNA
DE ligase) (MetRS).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Denizciak M., Miranda M.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + tRNA(Met) = AMP +
CC di-phosphate + L-methionyl-tRNA(Met).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- SIMILARITY: Belongs to the class-I aminoacyl-tRNA synthetase
CC family.
CC -1- SIMILARITY: Contains 1 tRNA-binding domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF040700; AAC99620.1; -.
CC HSSP; Q12904; 1FL0.
CC Gramene; Q9ZTS1; -.
CC InterPro; IPR008224; MetRS dimerising.
CC InterPro; IPR008994; Nucleic acid OB.
CC InterPro; IPR002300; tRNA-synt_1a.
CC InterPro; IPR001412; tRNA-synt_1.
CC InterPro; IPR002304; tRNA-synt_met.
CC InterPro; IPR002547; tRNA_bind.
CC InterPro; IPR009080; tRNA-synt_1.
CC Pfam; PF00133; tRNA-synt_1.
CC Pfam; PF01588; tRNA_bind.
CC PIRSF; PIRSF001528; MetRS dimerising; 1.
CC PRINTS; PR01041; TRNASYNTHMET.
CC TIGRFAMs; TIGR00398; metG; 1.
CC PROSITE; PS00178; AA tRNA_LIGASE_I; 1.
CC PROSITE; PS00886; TRBD; 1.
CC Aminoacyl-tRNA synthetase; ATP-binding; Ligase; Protein biosynthesis;
CC RNA-binding; tRNA-binding.
CC DOMAIN 4 11 Poly-Pro.
CC SITE 28 38 "HIGH" region.
CC SITE 350 354 "KMSKS" region.
CC BINDING 353 353 ATP (By similarity).
CC DOMAIN 642 745 tRNA-binding.
CC SEQUENCE 804 AA; 89716 MW; A87E8ABBD419D440 CRC64;

Query Match 32.9%; Score 517; DB 1; Length 804;
Best Local Similarity 38.1%; Pred. No. 9.3e-22;
Matches 117; Conservative 53; Mismatches 79; Indels 58; Gaps 9;

QY 35 KAILQATLREKKL-----RVENAKLKE-----IEELKQELQAEITQ 73
DB 527 EVLLQLNMTPEESLFCDDKGEIAKAKRPFVSGAGHKIGKPSPLFKELKDVEVES----- 582

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Qy 74 GVKQIAFPSPGTPPLHANGMWSENVIQSTAVTTVSSGK--EIQKGGTGDEKKAKEIKKG 131
Db 583 -----PRNKFAGSQAERSKKAQADAEAKKVDKLKG-----TKLSDGG 620
Qy 132 EKKEKKQOISAGSADSK----PIDVSRDLIRIGCIITARKHPDADSLRYVEVDVGEIAPR 187
Db 621 QKKEQKQS--GGSKSKNAEVDVTAKLDIRVGLIRKAQKHPDADSLRYVEIDVGEAPR 678
Qy 188 TVVSGLVNHPLEQONRQVILLCNLKPAMRGVLSOAMVWCASSPZ--KIEILLAPNGS 245
Db 679 TVVSGLVKFTPLEEQNRKVCVLCNLKPVAMRGKISHAMVLAASNEHDHTKVELVEPPESA 738
Qy 246 VPGDRITFDAPPGPDDELNPKKIWEQIOPLDHLTNDCEVATYKGVPEVKGKGVCAQCT 305
Db 739 AVGERVTFAGYSGEPEASLNKSKTWKLSADLHNSGELVACYKQDVFTTSA-GVCKVKS 797
Qy 306 MSNSGIK 312
Db 798 IASGEIR 804

RESULT 10
O62542 ID O62542 PRELIMINARY; PRT; 149 AA.
AC O62542:
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Endothelial-monocyte-activating polypeptide related protein.
GN Name=SWAPR1;
OS Geodia cydonium (Sponge).
OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
OC Astrophorida; Geodiidae; Geodia.
OX NCBI_TaxID=6047;
RN 1:
RP SEQUENCE FROM N.A.
RX MEDLINE=98184040; PubMed=9523439; DOI=10.1098/rspb.1998.0311;
RA Pahler S., Krasko A., Schuetz J., Mueller I.M., Mueller W.E.G.;
RT "Isolation and characterisation of the cDNA, encoding a potential
RT morphogen from the marine sponge Geodia cydonium that is conserved in
RT higher Metazoa."
RL Proc. R. Soc. Lond., B, Biol. Sci. 265:421-425(1998).
DR EMBL; Y14947; CAA75164.1; -.
DR HSPF; Q12904; 1F20.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0000049; F:RNA binding; IEA.
DR InterPro; IPR008994; Nucleic acid_OB.
DR InterPro; IPR02547; tRNA_bind.
DR Pfam; PF01588; tRNA_bind.1.
DR PROSITE; PS50886; TRBD; 1.
SQ SEQUENCE 149 AA; 16499 MW; 61272889BE17C7EF CRC64;

Query Match
Best Local Similarity 31.8%; Score 499.5; DB 2; Length 149;
Matches 92; Conservative 24; Mismatches 31; Indels 1; Gaps 1;

Qy 157 LRICITITARKHPDADSLRYVEVDVGEIAPRTVVSGLVNHPLEQONRQVILLCNLKP 216
Db 1 MRIGRITSVERHPDADTLVVEQIDVGEKPRTCVGLVTHVAITMNRLVVLVLCNLPV 60

Qy 217 KMRGVLSQVMWCASSPEKTEILAPNGSVPGDRITFDAPGEPDKEINPKKIWEQIO 276
Db 61 KMRGVTSEAMVMWCASSPENIEILPDPSVPGDRVFTFTGYTSPDTQLNPKKRVFTVQ 120

Qy 277 DLHNTDECVATYKGVPEVKGKGVCAQ 304
Db 121 DFLVNESGVATYRGIPLOWVR-VCAAQ 147

RESULT 11
SYM_ARATH ID_SYM_ARATH STANDARD; PRT; 797 AA.
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AC Q9SVN5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Probable methionyl-tRNA synthetase (EC 6.1.1.10) (Methionine--trNA
DE ligase) (MetRS).
GN OrderedLocusNames=At4g13780; ORFNames=F18A5.170;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN 1:
RP SEQUENCE FROM N.A.
RX STRAIN=cv. Columbia;
RX MEDLINE=20083488; PubMed=10617198; DOI=10.1038/47134;
RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
RA Pohl T., Dueterhoeft A., Stiekema W., Entian K.-D., Terryn N.,
RA Harris B., Ansoorge W., Brandt P., Grivell L.A., Rieger M.,
RA Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
RA Kreis M., Delsen M., Puigdomenech P., Watson M., Schmidtheini T.,
RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,
RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
RA Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
RA Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
RA Weitzenecker T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA Bernaisser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA De Keyser A., Buysshaert C., Gielen A., Villarroel R., De Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Quail M.A., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
RA Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Borkova D., Bloecker H., Scharfe M., Grimm M., Loehner T.-H.,
RA Dose S., de Haan M., Maarsee A.C., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fartmann B., Graendath K., Dauner D., Herzl A.,
RA Neumann S., Argirou A., Vitale D., Liguori R., Piravandi E.,
RA Massenet O., Quigley F., Clabaud G., Muendlein A., Felber R.,
RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Chefod F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Barges M., Terol J., Torres A.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse C.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bielke C.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Parnell L., Dedhia N., Ghoj L., Schutz K., Huang E., Spiegler L.,
RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.W.,
RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,
RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Tili S.,
RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
RA Chen E., Maria M.A., Martienssen R., McCombie W.R.;
RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
RT thaliana."
RL Nature 402:769-777(1999).
CC -I- CATALYTIC ACTIVITY: ATP + L-methionine + tRNA(Met) = AMP +
CC diphosphate + L-methionyl-tRNA(Met).
CC -I- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -I- SIMILARITY: Belongs to the class-I aminoacyl-tRNA synthetase
CC family.
CC -I- SIMILARITY: Contains 1 tRNA-binding domain.
CC
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DR EMBL; AL035528; CAB36842.1; -.
DR EMBL; AL161537; CAB78420.1; -.
DR PIR; T05247; T05247.
DR HGSP; Q12904; 1E7Z.
DR GeneFarm; 2798; -.
DR InterPro; IPR008224; MetRS dimerising.
DR InterPro; IPR008994; Nucleic acid OB.
DR InterPro; IPR002300; tRNA-synt_1a.
DR InterPro; IPR001412; tRNA-synt_1.
DR InterPro; IPR002304; tRNA-synt met.
DR InterPro; IPR002547; tRNA bind.
DR InterPro; IPR009080; tRNA-synt_1a_bind.
DR Pfam; PF00133; tRNA-synt_1.
DR Pfam; PF01588; tRNA bind; 1.
DR PIRSF; PIRSF001528; MetRS dimerising; 1.
DR PRINTS; PR01041; TRNASYNTHET.
DR TIGRFAMs; TIGR00398; metG; 1.
DR PROSITE; PS00178; AA tRNA_LIGASE_I; 1.
DR PROSITE; PS00886; TRBD; 1.
DR Aminoacyl-tRNA synthetase; ATP-binding; Ligase; Protein biosynthesis;
KW RNA-binding; tRNA-binding.
FT SITE 26 36 "HIGH" region.
FT SITE 348 352 "KMSKS" region.
FT BINDING 351 351 ATP (By similarity).
FT DOMAIN 635 738 tRNA-binding.
SQ SEQUENCE 797 AA; 89853 MW; B0F523C2E0C1017F CRC64;

Query Match 31.7%; Score 499; DB 1; Length 797;
Best Local Similarity 52.9%; Pred. No. 1e-20;
Matches 101; Conservative 31; Mismatches 51; Indels 8; Gaps 3;

Qy 124 KEIEKKEKKEKQKQSTAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEE 183
Db 613 KQKASSKGGKPKQ-----PAADREITMARLDIRVGKIVKAEKHPKADALYVEIDVG 667
Qy 184 IAPRTVSLGNVHPLEQNMQRNVILLCNLKPARKRGVLSQAMVWCASSPE--KIEILAP 241
Db 668 GEIRTVWSGLVKYIPLSEMQNRVVCVLCNLKPARKRDIVSQAMVLAASSDGSVELVEP 727
Qy 242 PNGSPGDRITFDAPFGPDRELKPKKIWEIQPDLTNDCEVATYKGVFEVKGKGV 301
Db 728 PKTANIGERVTPPGFEGEPDVLAPKKKWETLLVLDNLTKENLVACYKQDVEFTSA-GVC 786
Qy 302 RAQTMNSNGIK 312
Db 787 KVSSISNGTIR 797

RESULT 12
Q6TGS6 PRELIMINARY; PRT; 529 AA.
AC Q6TGS6
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Tyrosyl-tRNA synthetase.
GN Name=vars; Synonyms=VARS.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney marrow;
RA Song H.Y., Wu X.Y., Sun X.J., Zhou Y., Liu T.X., Deng M., Zhang G.W.,
RA Sheng Y., Chen Y., Ruan Z., Jiang C.L., Fan H.Y., Zou L.I.,
RA Kanki J.P., Look A.T., Chen Z.
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
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DR EMBL; AY398430; AAQ97863.1; -.
DR ZFIN; ZDB-GENE-030425-2; Yars.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0000049; F:tRNA binding; IEA.
DR GO; GO:0004831; F:tyrosine-tRNA ligase activity; IEA.
DR GO; GO:0006437; P:tyrosyl-tRNA aminoacylation; IEA.
DR InterPro; IPR008437; P:tyrosyl-tRNA aminoacylation; IEA.
DR InterPro; IPR008232; EMAP11.
DR InterPro; IPR008994; Nucleic acid OB.
DR InterPro; IPR002305; tRNA-synt_1b.
DR InterPro; IPR002547; tRNA bind.
DR Pfam; PF00579; tRNA-synt_1b; 1.
DR Pfam; PF01588; tRNA bind; 1.
DR PIRSF; PIRSF005381; EMAP11; 1.
DR PRINTS; PR01040; TRNASYNTHYR.
DR TIGRFAMs; TIGR00234; tyrS; 1.
DR PROSITE; PS00886; TRBD; 1.
DR Aminoacyl-tRNA synthetase.
KW Aminoacyl-tRNA synthetase.
SQ SEQUENCE 529 AA; 59505 MW; C3314003813B9336 CRC64;

Query Match 28.8%; Score 453.5; DB 2; Length 529;
Best Local Similarity 39.8%; Pred. No. 2.7e-18;
Matches 123; Conservative 43; Mismatches 78; Indels 65; Gaps 14;

Qy 44 EEKRLRV--ENAKLKKEIEELKQELIOAEIQNG-----VKQIAPPSGTPPLHANSWVS---- 93
Db 228 EESKIDLLDNQDVKKLKKAFCEPGNVE--NGVLSFVKHVLV----PLHSEFVIKRDPK 282
Qy 94 -----ENVIQSTAVTVSSGTYKEQIKGGTGDEK-----KAKKIEKKKKEKE 135
Db 283 FGGDKVYTDPEVEKDFAA-----EQIH--PGDLKASVELALNKLLOPIRKFFSPE 332
Qy 136 -KKQKQSTA-----GSADSKP-----IDVSRDLRIGCIITARKHPDADSLYVEE 178
Db 333 LKLTTSAYPEPKKNGKAGKGNPKQTDDDEVIPSRDLDIRGVISVEKHPDADSLYLEK 392
Qy 179 VDVEGIAPRTVWSGLNVHPLEQNMQRNVILLCNLKPARKRGVLSQAMVWCAS---SPEK 235
Db 393 IDVGEQPRTVWSGLVAVITEEQQLDRLLVLLCNLKPQKMGIESQAMVLCASIEGEPRK 452
Qy 236 IEILAPNGSPGDRITFDAPF-PGEPKELNPKKIWEIQPDLTNDCEVATYKGVFPPE 294
Db 453 VEPLDPPGSAAGRVYVEGVESGKPDDELKPKKVFELQVDLKI SGFEFVAQMKQNLN 512
Qy 295 VK-GKGVCR 302
Db 513 TKLAGRITCK 521

RESULT 13
Q6DFZ7 PRELIMINARY; PRT; 529 AA.
AC Q6DFZ7
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Tyrosyl-tRNA synthetase.
GN Name=Yars;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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94 ENVI-----QSTAVTTVSSGTEKIQKGGTDEKKA-----KEKIEKKG 131
 273 EFVILRDEKGNKNTYATLDEKFADEVV-HPGDLKNSVEVALNKLLDPIREKENTPA 331
 132 EKK-----EKKQSQSIAGSA-DSKPIDV--SRLLDLRIGCIITAKRHPDADSLYVEEV 179
 332 LKLLSSAAYPDPSKQKPAVKGPAKNSPEEIPSRLLDIRVGKVISVDKHPDADSLYVEKI 391
 180 DVGEIARTVVGSLVNHVPLEQMONRMVILLCNLKPAMRGVLTSGQMMVCASSP---EKI 236
 392 DVGEAEPRTVVGSLVNFVPELQDLRVVLCNLKPKQKGVKSGQMLLCLASVGVNRKV 451
 237 EILAPPNGSVGDRITTFDAF-PGSPDKELNPKKIWEIQIDPLTNDCEVATYKGVPFV 295
 452 EPLDPPAGSARGFVFKYKGVKQDEELPKPKVFEKLQADFKISDEYIAQWKQTFMT 511
 296 K-GKGVCRBA 303
 512 KMGSVSCKS 520

RESULT 15
 SYIC HUMAN
 ID SYIC HUMAN STANDARD; PRT; 527 AA.
 AC P54577; O43276;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Tyrosyl-tRNA synthetase, cytoplasmic (EC 6.1.1.1) (Tyrosyl--tRNA
 ligase) ("tyrRS").
 GN Name=VARS;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96133898; PubMed=8552597; DOI=10.1073/pnas.93.1.166;
 RA Ribas de Fouplana L., Frugier M., Quinn C.L., Schimmel P.;
 RT "Evidence that two present-day components needed for the genetic code
 appeared after nucleated cells separated from eubacteria."
 RL Proc. Natl. Acad. Sci. U.S.A. 93:166-170 (1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97306356; PubMed=9162081; DOI=10.1074/jbc.272.22.14420;
 RA Kleeman T.A., Wei D., Simpson K.L., First E.A.;
 RT "Human tyrosyl-tRNA synthetase shares amino acid sequence homology
 with a putative cytokine."
 RL J. Biol. Chem. 272:14420-14425 (1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bone, and Lung;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny N.J., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 [4]
 RL SEQUENCE OF 1-15.
 RN TISSUE=Platelet;
 RC MEDLINE=22608298; PubMed=12665801; DOI=10.1038/nbt810;
 RX Gevaert K., Goethals M., Martens L., Van Damme J., Staes A.,
 RA Thomas G.R., Vandekerckhove J.;
 RT "Exploring proteomes and analyzing protein processing by mass
 spectrometric identification of sorted N-terminal peptides."
 RL Nat. Biotechnol. 21:566-569 (2003).
 RN [5]
 RP SEQUENCE OF 1-15, AND ACETYLATION SITE GLY-1.
 RC TISSUE=B-cell lymphoma;
 RN Bienvenut W.V.;
 RL Unpublished observations (OCT-2004).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (1.18 ANGSTROMS) OF 3-341.
 RX PubMed=12427973; DOI=10.1073/pnas.242611799;
 RA Yang X.L., Skene R.J., McRee D.E., Schimmel P.;
 RT "Crystal structure of a human aminoacyl-tRNA synthetase cytokine."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:15369-15374 (2002).
 CC -1- CATALYTIC ACTIVITY: ATP + L-tyrosine + tRNA(Tyr) = AMP +
 CC diphosphate + L-tyrosyl-tRNA(Tyr).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: Belongs to the class-I aminoacyl-tRNA synthetase
 CC family.
 CC -1- SIMILARITY: Contains 1 tRNA-binding domain.
 CC -1- CAUTION: Ref.1 sequence differs from that shown due to a
 CC frameshift in position 353.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: U40714; AAB39406.1; ALT_FRAME.
 CC EMBL: U89436; AAB88409.1; --
 CC EMBL: BC001933; AAH01933.1; --
 CC EMBL: BC004151; AAH04151.1; --
 CC EMBL: BC016689; AAH16689.1; --
 CC PDB: 1N3L; X-ray; A=1-371.
 CC PDB: 1NTG; X-ray; A/B/C/D=358-527.
 CC PDB: 1Q11; X-ray; A=1-371.
 CC Genew; HGNC:12840; YARS.
 CC H-invDB; HIX0000381; --
 CC MIM; 603623; --
 CC GO; GO:0005737; C:cytoplasm; TAS.
 CC GO; GO:0005615; C:extracellular space; TAS.
 CC GO; GO:0005625; C:soluble fraction; TAS.
 CC GO; GO:0005625; F:interleukin-8 receptor binding; TAS.
 CC GO; GO:0005153; F:tyrosine-tRNA ligase activity; TAS.
 CC GO; GO:0006915; P:apoptosis; TAS.
 CC GO; GO:0006437; P:tyrosyl-tRNA aminoacylation; TAS.
 CC InterPro; IPR008994; Nucleic acid OB.
 CC InterPro; IPR002305; tRNA-synt_1b.
 CC InterPro; IPR004412; tRNA-synt_1.
 CC InterPro; IPR002547; tRNA-bind.
 CC InterPro; IPR002307; Tyr_tRNA-synt_1b.
 CC Pfam; PF01588; tRNA-bind; 1.
 CC Pfam; PF00579; tRNA-synt_1b; 1.
 CC PRINTS; PR01040; TRNASYNTHYR.
 CC TIGRFAMs; TIGR00234; tyrS; 1.
 CC PROSITE; PS00178; AA TRNA_LIGASE_I; FALSE_NEG.
 CC PROSITE; PS00886; TRBD; 1.
 CC 3D-structure; Acetylation; Aminoacyl-tRNA synthetase; ATP-binding;
 CC Direct protein sequencing; Ligase; Protein biosynthesis; RNA-binding;
 CC tRNA-binding.
 CC INIT MET 0 0
 CC MOD RES 1 1 N-acetylglucosamine.
 CC SITE 43 51 "HIGH" region.

Qy	230	ASSP---EKIELAPPNGSVFGDRITFDAP-PGEPPDKELNPKKIIWGOIQPDLLHTNDECV	288
Db	442	ASIEGINRQVEPLDPPAGSAFGEHVFVKGYEKGPDEELKPKKVFKEKLQADFKISBECI	501
Qy	286	ATYKGVPPPEVK-GKGVCR	303
Db	502	AOWKQTNFWTKLGSISCKS	520

Search completed: August 3, 2005, 21:57:20

Job time : 177 secs

Qy	230	ASSP---EKIEILAPPNGSVPGDRITFDAF-PGEPDKELNPKKKIWEQIQPDLHTNDECV	285
Db	442	ASIEGINRQVEPLDPPAGSAPGEHVFKGYEKQGPDEELKPKKKVFEKLQADFKESECI	501
Qy	286	ATYKGVPPFEVK-GKGVCR	303
Db	502	AQWKQTNFTKLGSI	520

Search completed: August 3, 2005, 21:57:20
Job time : 177 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2005, 21:46:39 ; Search time 41 Seconds
(without alignments)
732.186 Million cell updates/sec

Title: US-10-623-567A-1

Perfect score: 1573

Sequence: 1 MANNDVAVLKRLQKGAADQ.....FEVKGKGVCAQTMSNSGIK 312

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1546	98.3	310	B55053	endothelial monocy
2	1343	85.4	310	A55053	endothelial monocy
3	564	35.9	917	T22898	hypothetical prote
4	499	31.7	797	T05247	methionine-trna li
5	429	27.3	376	S64113	ARC1 protein - yea
6	400.5	25.5	440	C84832	probable methionyl
7	343	21.8	273	T47822	hypothetical prote
8	223.5	14.2	722	B55074	methionyl-trna syn
9	216	13.7	723	D71091	methionine-trna li
10	205	13.0	616	SYTWT	methionine-trna li
11	198.5	12.6	110	C85968	probable trna synt
12	198.5	12.6	110	D91123	hypothetical 12.3
13	194.5	12.4	110	G85095	methionine-trna li
14	191	12.1	658	D69431	methionine-trna li
15	185.5	11.8	629	E72297	methionine-trna li
16	183.5	11.7	650	A64572	methionine-trna li
17	182.5	11.6	651	F64457	methionine-trna li
18	178.5	11.3	811	E71281	methionine-trna li
19	177	11.3	660	E83656	methionyl-trna syn
20	170	10.8	656	H71867	methionine-trna li
21	168.5	10.7	114	F82090	methionyl-trna syn
22	168.5	10.7	681	C75395	methionyl-trna syn
23	168	10.7	734	B70173	methionine-trna li
24	159.5	10.1	664	A11459	methionyl-trna syn
25	158	10.0	664	S66067	methionine-trna li
26	156.5	9.9	665	D95091	methionyl-trna syn
27	156.5	9.9	679	H97958	methionine-trna li
28	155.5	9.9	664	AB1097	methionyl-trna syn
29	151	9.6	644	A97268	methionyl-trna syn

ALIGNMENTS

RESULT 1

B55053

endothelial monocyte-activating protein II precursor - human

C:Species: Homo sapiens (man)

C:Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Dec-2002

C:Accession: B55053

R:Kao, J.; Houck, K.; Fan, Y.; Haehnel, I.; Libutti, S.K.; Kayton, M.L.; Grikscheit, T.; J.; Stern, D.M.

J. Biol. Chem. 269, 25106-25119, 1994

A:Title: Characterization of a novel tumor-derived cytokine. Endothelial-monocyte activa

A:Reference number: A55053; MUID:95014290; PMID:7929199

A:Accession: B55053

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-310 <KAO>

A:Cross-references: CB:U10117

C:Superfamily: endothelial monocyte-activating polypeptide II precursor (pro-EMAP II)

Query Match 98.3%; Score 1546; DB 2; Length 310;

Best Local Similarity 99.0%; Pred. No. 1.9e-87;

Matches 309; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

Qy	1	MANNDVAVLKRLQKGAADQII EYLKQVSLLEKAILQATLREKKLRVENAKLKKEIE	60
Db	1	MANNDVAVLKRLQKGAADQII EYLKQVSLLEKAILQATLREKKLRVENAKLKKEIE	60
Qy	61	ELKQELIQAEIQNGVKQIAFPSCGPLHANSVSENVIOSTAVTTVSSGKQIKGTGDE	120
Db	61	ELKQELIQAEIQNGVKQIRFPSPGPLHANSVSENVIOSTAVTTVSSGKQIKGTGDE	118
Qy	121	KKAKEKTEKKEKKEKQOOSTAGSADSKPIDVSRDLRLIGCIIITARKHPDADSLYVEEVD	180
Db	119	KKAKEKTEKKEKKEKQOOSTAGSADSKPIDVSRDLRLIGCIIITARKHPDADSLYVEEVD	178
Qy	181	VGEIAPRTVTVSGLVNHPLEQQRNRMVILLCNLPAKMRGVLSQLAMVNCASSPEKIEILA	240
Db	179	VGEIAPRTVTVSGLVNHPLEQQRNRMVILLCNLPAKMRGVLSQLAMVNCASSPEKIEILA	238
Qy	241	PPNGSVPGDRITFDAPGEPDKELNPKKKIWEIQPDLHTNDECVCATYKGVPPFEVKGKV	300
Db	239	PPNGSVPGDRITFDAPGEPDKELNPKKKIWEIQPDLHTNDECVCATYKGVPPFEVKGKV	298
Qy	301	CRAQTMSNSGIK 312	
Db	299	CRAQTMSNSGIK 310	

RESULT 2

A55053

endothelial monocyte-activating protein II precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004

C;Accession: A55053; A44032
R;Kao, J.; Houck, K.; Pan, Y.; Haehnel, I.; Libutti, S.K.; Kayton, M.L.; Grikscheit, T.; J.; Stern, D.M.
J. Biol. Chem. 269, 25106-25119, 1994
A;Title: Characterization of a novel tumor-derived cytokine. Endothelial-monocyte activating factor protein-1
A;Reference number: A55053; MUID:95014290; PMID:7929199
A;Accession: A55053
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-310 <KAO>
A;Cross-references: UNIPROT:P31230; GB:U10118; NID:G498911; PIDN:AAA62203.1; PID:G498912
R;Kao, J.; Ryan, J.; Brett, G.; Chen, J.; Shen, H.; Fan, Y.G.; Godman, G.; Familletti, P.G.; J. Biol. Chem. 267, 20239-20247, 1992
A;Title: Endothelial monocyte-activating polypeptide II. A novel tumor-derived polypeptide
A;Reference number: A44032; MUID:93015897; PMID:1400342
A;Accession: A44032
A;Molecule type: protein
A;Residues: 145-158, 'X', 160-164 <KAO>
A;Experimental source: methylcholanthrene A fibrosarcoma cells
A;Note: sequence extracted from NCBI backbone (NCBIP:115676)
C;Superfamily: endothelial monocyte-activating polypeptide II precursor (pro-EMAP II)

Query Match 85.4%; Score 1343; DB 2; Length 310;
Best Local Similarity 85.9%; Pred. No. 4.7e-75;
Matches 269; Conservative 13; Mismatches 27; Indels 4; Gaps 3;

Qy 1 MANDAVLKRLEQKGAADQIIIEYLKQOVSLLEKAKILQATLRREKRLRVENAKLKEIE 60
Db 1 MATNDVAVLKRLEQKGAADQIIIEYLKQOVALLKEKAILQATLRREKRLRVENAKLKEIE 60

Qy 61 ELKQELQAEITONGVKQIAAPSGPLHANSMVSENVQSTAV-TTVSSGTEKQIKGGTGD 119
Db 61 ELKQELQAEITONGVKQIAAPSGPLHANSMVSENVQSTAV-TTVSSGTEKQIKGGTGD 119

Qy 120 EKKAKEIEKKGEKKKQKQSIAGSADSKPTIDVSRDLRIGCIITARKHPDADSLYVEEV 179
Db 120 EKKAKEIEKKGEKKKQKQSIAGSADSKPTIDVSRDLRIGCIITARKHPDADSLYVEEV 179

Qy 180 DVGSIAPRTVSGLVNHVPLEQMNRMVLLCNLKPAMRGVLSQAMVMCASSPEKTEIL 239
Db 180 DVGSIAPRTVSGLVNHVPLEQMNRMVLLCNLKPAMRGVLSQAMVMCASSPEKTEIL 239

Qy 240 APPNGSVPGDRITFDAPGEPDKELNPKKIWEQIQDPLHTNDECVATYKGVPPKGG 299
Db 240 APPNGSVPGDRITFDAPGEPDKELNPKKIWEQIQDPLHTNDECVATYKGVPPKGG 299

Qy 300 VCRAQTMSNSGIK 312
Db 300 VCRAQTMSNSGIK 310

RESULT 3
T22898
hypothetical protein F58B3.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
A;Reference number: T22898
R;Harris, B.
submitted to the EMBL Data Library, May 1996
A;Accession: T22898
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-917 <WIL>
A;Cross-references: UNIPROT:Q20970; EMBL:Z73427; PIDN:CAA97803.1; GSFDB:GN00022; CESP:F58B3
A;Experimental source: clone F58B3
C;Genetics:
A;Gene: CESP:F58B3.5
A;Map position: 4
A;Introns: 27/2; 135/2; 620/1; 655/1; 874/3
C;Superfamily: methionyl-tRNA synthetase, dimer-forming

Query Match 35.9%; Score 564; DB 2; Length 917;

Best Local Similarity 42.3%; Pred. No. 6e-27;
Matches 135; Conservative 52; Mismatches 100; Indels 32; Gaps 8;

Qy 1 MANDAVLKRLEQKGAADQIIIEYLKQOVSLLEKAKILQATLRREKRLRVENAKLKEIE 59
Db 624 MASTAAFE-LEQKAKVISLIAQNLK---FDQAKALF--TRNQLRLOGENKQLTIDV 677

Qy 60 EELKQELQAEITONGVKQIAAP--SGTPLHANSMVSENVQSTAVTVSSGTEKQIKGGT 117
Db 678 KTLQHQLELETAAGIKQVPPVSVCTP-----TPTSTPASGLITE----- 718

Qy 118 GDEKKAKEIEKKGEKKKQKQSIAGSADSKP-----IDVSRDLRIGCIITARKHPDAD 173
Db 719 APKKEAPSTPAPSEPKKAKQKGGKGAAPVDDTIDVGRDLWRVGRRIKCEKHPDADA 778

Qy 174 LYVEEDVGVHAIAPRTVSGLVNHVPLEQMNRMVLLCNLKPAMRGVLSQAMVMCASSP 233
Db 779 LYVEQIDVGVHAIAPRTVSGLVNHVPLEQMNRMVLLCNLKPAMRGVLSQAMVMCASSP 838

Qy 234 EKTEILAPPNGSVPGDRITFDAPGEPDKELNPKKIWEQIQDPLHTNDECVATYKGVPP 293
Db 839 DKVEIMEVPADSKPGTFVCPPTTHRDEQNLNPKKIWEQIQDPLHTNDECVATYKGVPP 898

Qy 294 EVKGGKGVCRQAQTMNSGIK 312
Db 899 LIGSESKMTAPTTLRGVHVK 917

RESULT 4
T05247
methionine-tRNA ligase homolog F18A5.170 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T05247
R;Bevan, M.; Weber, N.; Grueninger, D.; Schmidheini, T.; Bancroft, I.; Mewes, H.W.; Mayer, R.; Mayhew, M.W.; submitted to the Protein Sequence Database, February 1999
A;Reference number: Z15405
A;Accession: T05247
A;Molecule type: DNA
A;Residues: 1-797 <BEV>
A;Cross-references: UNIPROT:Q9SVNS; EMBL:AL035528
A;Experimental source: cultivar Columbia; BAC clone F18A5
C;Genetics:
A;Map position: 4
A;Introns: 40/1; 88/2; 139/3; 191/3; 268/3; 316/3; 347/1; 382/3; 423/1; 460/3; 482/3; 52/3
C;Superfamily: methionyl-tRNA synthetase, dimer-forming

Query Match 31.7%; Score 499; DB 2; Length 797;
Best Local Similarity 52.9%; Pred. No. 4.8e-23;
Matches 101; Conservative 31; Mismatches 51; Indels 8; Gaps 3;

Qy 124 KEKIEKKGEKKKQKQSIAGSADSKPTIDVSRDLRIGCIITARKHPDADSLYVEEDVGE 183
Db 613 KQKASSKGGKPKPQ-----PAADREITMARLDIRVGIKVAEKHPKADALYVEEDVGG 667

Qy 184 IAPRTVSGLVNHVPLEQMNRMVLLCNLKPAMRGVLSQAMVMCASSPE--KIETLAP 241
Db 668 GEIRTVSGLVNPKYIPEEMQNRMVLCNLKPAMRDIVSQAMVLAASDGGSKVELVEP 727

Qy 242 PNGSVPGDRITFDAPGEPDKELNPKKIWEQIQDPLHTNDECVATYKGVPPFVKGGVC 301
Db 728 PKTANIGERTVTFPGFEGEPDVLNPKKVVETLLVDLNTKENLVACYKDVFFTTSA-GVC 786

Qy 302 RAQTMNSGIK 312
Db 787 KVSSISNGTIR 797

RESULT 5
S64113
ARCI protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: G4p1 protein; protein G3085; protein YGL105w

C;Species: Saccharomyces cerevisiae
C;Date: 17-May-1996 #sequence revision 17-May-1996 #text_change 09-Jul-2004
C;Accession: S64113; S69425; S72274
R;Castagnoli, L.; Paoluzi, S.; Minenkova, O.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64112
A;Accession: S64113
A;Molecule type: DNA
A;Residues: 1-376 <CAS>
A;Cross-references: UNIPROT:P46672; EMBL:P46672; NID:g1322627; PIDN:CAA96812.1; PID:g1322627
A;Experimental source: strain S288C
R;Castagnoli, L.; Paoluzi, S.; Minenkova, O.
submitted to the EMBL Data Library, April 1996
A;Reference number: S69417
A;Accession: S69425
A;Molecule type: DNA
A;Residues: 1-376 <CW>
A;Cross-references: EMBL:X97644; NID:g1310710; PIDN:CAA66247.1; PID:g1310719
R;Simos, G.; Segref, A.; Fasiolo, F.; Hellmuth, K.; Shevchenko, A.; Mann, M.; Hurt, E.C.
EMBO J. 15, 5437-5448, 1996
A;Title: The yeast protein Arcip binds to tRNA and functions as a cofactor for the methionyl-tRNA synthetase
A;Reference number: S72274; MUID:97050848; PMID:8895587
A;Accession: S72274
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-376 <STM>
A;Cross-references: EMBL:X95481; NID:g1620459; PIDN:CAA64750.1; PID:g1620460
C;Genetics:
A;Gene: SGD:ARC1; G4P1
A;Cross-references: MIPS:YGL105w; SGD:S0003073
A;Map position: 7L
C;Complex: homodimer
C;Function:
A;Description: functions as a cofactor for methionyl- and glutamyl-tRNA synthetases
C;Superfamily: endothelial monocyte-activating polypeptide II precursor (pro-EMAP II)
C;Keywords: cytosol; homodimer

Query Match 27.3%; Score 429; DB 2; Length 376;
Best Local Similarity 42.7%; Pred. No. 3.7e-19;
Matches 105; Conservative 32; Mismatches 81; Indels 28; Gaps 9;

Qy 56 KKEIE--ELKQELQAEIQNGVQIAPPSGTPPLHANSMVSENIQSTAVTTVSSGTKEQ 112
Db 116 KLEINHDLDPHEVIE-----KKKAPAGGAADAAMAKADEVSK-----KAKQD 160

Qy 113 IKGTGDE---KKAKEIE-KKGEKK-----EKQSIAGSADSKPIDVSRDLRGICITA 165
Db 161 HPRGKPDDETLKGLREAAKAKAAKAAKQOQEQQNKAKPEK-KPSAIDFRVGFIOKA 219

Qy 166 RKHPDADSLYVEEDVVG-EIAPRTVSGLVNHPLEOMONRWILLCNLKPAMKRGVLSQ 224
Db 220 IKHPDADSLYVSTIDVGDEEGRTVCSGLVGHFPDADMOERYVVVVCNLPVNRGIKST 279

Qy 225 AMVMCASSPEKIEILAPPNGSVPGDRITFDAPGGE-PDKELNPKKKIWEIQPDLHTNDE 283
Db 280 AMVLGSSNDKVEFVEPPKSKAGDKVFFEGFGDEAPMKQLNPKKKIWEIHLQPHFTTNDG 339

Qy 284 CVATYK 289
Db 340 LEVIFK 345

RESULT 6
C84832
probable methionyl-tRNA synthetase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: C84832
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Unayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: C84832
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-440 <STO>
A;Cross-references: UNIPROT:Q7XJMR; GB:AE002093; NID:g4895232; PIDN:AA032818.1; GSPDB:GN
C;Genetics:
A;Gene: At2g40660
A;Map position: 2
C;Superfamily: endothelial monocyte-activating polypeptide II precursor (pro-EMAP II)

Query Match 25.5%; Score 400.5; DB 2; Length 440;
Best Local Similarity 35.6%; Pred. No. 2.5e-17;
Matches 105; Conservative 45; Mismatches 86; Indels 59; Gaps 9;

Qy 22 IEYLKQOVSLKKEKAILQATLRE-----EKKLKRVN-NAKLKEIEBELKQELQAEIQNG 74
Db 180 VNTIQNKEELSTLPAPVPLPFESFVPPKPAKIVETNSNKKAAE-----G 226

Qy 75 VKQIAPPSGTPPLHANSMVSENIQSTAVTTVSSGTKEQIKGGTGDEKKAKEIKKGEKK 134
Db 227 VKPVDKPDVQF-----QLGTTK-----TRPEPCKNAAKEKDAKK 261

Qy 135 EKQOSIAGSADSKP-----IDVSRDLRLGICITARKHPDADSLYVEEDVGEIAPRT 188
Db 262 EKKK-----PAEPEPAKKEAELSVSLNIIQVGLIRKAWKHPADSLSLVEEDVGEIKVRQ 316

Qy 189 VVSGLVNHPLEOMONRWILLCNLKPAMKRGVLSQAMVMCASSPEK--EILAPPNGSV 246
Db 317 VVSLAKFCSPEDLTNLVALITVVKPKGLRDVMSQGLVLCASSEDHSVVEPLPPAGAK 376

Qy 247 PGDRITFDAPFGEPEKELNPKKKIWEIQPDLHTNDECVATYKGVPPFVKGGKVC 301
Db 377 PGRVSFSGIEGKPEDVLPKPKKLEKITPGLYTDENGVAITYKGIQF-MTSAGPC 430

RESULT 7
T47822
hypothetical protein F24G16.250 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 17-Feb-2003
C;Accession: T47822
R;D'Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Lemcke, K.;
submitted to the Protein Sequence Database, February 2000
A;Reference number: Z24477
A;Accession: T47822
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-273 <DAN>
A;Cross-references: EMBL:AL138647
A;Experimental source: cultivar Columbia; BAC clone F24G16
C;Genetics:
A;Map position: 3
A;Introns: 157/3; 226/3
A;Note: F24G16.250
C;Superfamily: endothelial monocyte-activating polypeptide II precursor (pro-EMAP II)

Query Match 21.8%; Score 343; DB 2; Length 273;
Best Local Similarity 37.8%; Pred. No. 4.6e-14;
Matches 84; Conservative 40; Mismatches 56; Indels 40; Gaps 7;

Qy 101 AVTTVSSGTKEQIKGGTGDEKKAKEIKKGEKKKQOSIAGSADSKPIDVSRDLRLG 160
Db 80 AGTTVSA-----DESEKKSE-SQKEENVKETA-----NLLDIKVG 114

Qy 161 CIITARKHPDADSLYVEEDVGEIAPRTVSGLVNHPLEOMONRWILLCNLKPAMKRG 220
Db 115 RIVKAWQHEEADSLYVEEDVGEIAPRTVSGLVNHPLEOMONRWILLCNLKPAMKRG 174

Qy 221 VLSQAMVMCAS--SPEKIEILAPPNGSVPGDRITFDAPFGEPEKELN-----KKK 269
Db 175 VKSCMLLAADAHAENVELLPVPEGSVPGDRVWFG---NEEDLEQLPEAPPNKKVQKKK 231


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| : | :: | | : | : | : || | : 
Db      629 SRGMILAAEXDGRKAVLLTPEKEVEPGTRV 657

RESULT 15
E72297
methionine-tRNA ligase (EC 6.1.1.10) - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: E72297
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; PMID:10360571
A;Accession: E72297
A>Status: preliminary
A:Molecule type: DNA
A;Residues: 1-629 <ARN>
A;Cross-references: UNIPROT:O33925; GB:AE001769; GB:AF000512; NID:g4981619; PIDN:AAD3616
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM1085
C;Superfamily: methionyl-tRNA synthetase, dimer-forming
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match          11.8%; Score 185.5; DB 2; Length 629;
Best Local Similarity 26.2%; Pred. No. 0.0005;
Matches 50; Conservative 46; Mismatches 72; Indels 23; Gaps 4;

Qy    83   GTPLHANSVMSENVIOSTAVTTVSSTGKEIQKGDTGDEKKAKEIE----- 128
Db     441  GTVLV-NSLEAVFKVALMTLPVMPDTSSEVFRRVSFEKPSEKHLENWGLPKGSTVIHG 499

Qy    129  ----KKGEKKEKQOSTAGSADSKPI---DVSRDLRIIGCIITARKHPDADSILYVEVDV 181
Db     500  EPFLPKIKDAKDFKWVETVSAEQNAITDDFSKDRLRIAKVLEAEKVPSRKLRLLIIDL 559

Qy    182  GEIAPRTVVSGLVNHVPLEQMQRNVILLCNLKPAMRGVLISQAWMCASSPEKIBILAP 241
Db     560  G-TREKRIVAGIAEHYPSELVGKLIVVANLPAKLMGIESQGMLLAASKGTLLRLTV 618

Qy    242  PNGSVPGDRIT 252
Db     619  DGEITPGAKVS 629

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XX PN WO200195927-A1.
XX PD 20-DEC-2001.
XX PF 14-JUN-2000; 2000WO-KR000630.
XX PR 14-JUN-2000; 2000WO-KR000630.
XX PA (INAG-) INAGENE CO LTD.
XX PI Kim S, Ko Y, Kim YS, Jo YJ;
XX DR WPI; 2002-098017/13.
XX DR N-PSDB; ABA94640.
XX PT Novel anti-tumor and anti-angiogenic agent of p43 comprises N-terminal domain and C-terminal domain containing eleven beta-strands forming a structural core and three flanking alpha-helices.
XX PS Claim 1; Fig 1; 35pp; English.
XX CC The invention provides an anti-tumor and anti-angiogenic agent of p43 consisting of two domains, the N-terminal domain (146 amino acids) and C-terminal domain (166 amino acids) containing 11 beta-strands forming a structural core and 3 flanking alpha-helices. p43 is useful as an anti-tumor and anti-angiogenic agent. p43 and its C-terminal cytokine domain (EMAP II) induce regression of fibrosarcoma in immunocompromised mouse while its N-terminal domain does not. p43 is a potent cytokine as determined by the induction of tumor necrosis factor-alpha (TNF-alpha), interleukin-6 (IL-6), IL-8 and matrix metalloproteinase-9 or by its activity of chemotaxis. The present sequence represents the human p43 polypeptide
XX SQ Sequence 312 AA;
Query Match 100.0%; Score 1573; DB 5; Length 312;
Best Local Similarity 100.0%; Pred. No. 1.6e-135;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MANNDVLRLEQKGAEADQII EYLKQOVSLLEKAILQATLREKKLRVENAKLKKIE 60
Db 1 MANNDVLRLEQKGAEADQII EYLKQOVSLLEKAILQATLREKKLRVENAKLKKIE 60
Qy 61 ELKQELIQAEIQNGVKQIAPPSGTPHANSMVSENVIOSTAVTTVSSGTEQIKGCTGDE 120
Db 61 ELKQELIQAEIQNGVKQIAPPSGTPHANSMVSENVIOSTAVTTVSSGTEQIKGCTGDE 120
Qy 121 KKAKEKIEKGEKKEKQOQSTAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEVD 180
Db 121 KKAKEKIEKGEKKEKQOQSTAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEVD 180
Qy 181 VGEIAPRTVSVGLVNHVPLEQMNRMVILLCNLKPAGKRGVLSQAMVNCASSPEKIEILA 240
Db 181 VGEIAPRTVSVGLVNHVPLEQMNRMVILLCNLKPAGKRGVLSQAMVNCASSPEKIEILA 240
Qy 241 PPGSVPGDRITFDAPFGEPEKELNPKKKIWEQIQPDLHTNDECVATYKGVPPFVKGV 300
Db 241 PPGSVPGDRITFDAPFGEPEKELNPKKKIWEQIQPDLHTNDECVATYKGVPPFVKGV 300
Qy 301 CQAQTMNSNGIK 312
Db 301 CQAQTMNSNGIK 312
RESULT 2
AAO29575
ID AAO29575 standard; protein; 312 AA.
XX AAO29575;
XX AAO29575;
XX 27-AUG-2003 (first entry)
XX

DS Human Pc240 protein.
XX Human; differentially regulated protein; prevention; therapy; vaccine;
KW prostate cancer; endothelial monocyte activating polypeptide II;
XX gene therapy; Pc240.
XX Homo sapiens.
XX OS
XX PN WO2003040331-A2.
XX PD 15-MAY-2003.
XX PF 07-NOV-2002; 2002WO-US035563.
XX PR 07-NOV-2001; 2001US-0331041P.
XX PR 07-NOV-2001; 2001US-0331042P.
XX PR 18-DEC-2001; 2001US-0340251P.
XX PR 07-JAN-2002; 2002US-0344791P.
XX PA (ORIG-) ORIGENE TECHNOLOGIES INC.
XX PI Sun Z, Li X, Jay G, Kovacs KP, Fan W;
XX DR WPI; 2003-449451/42.
XX DR N-PSDB; AAL60070.
XX PT New polynucleotide for diagnosing, staging, monitoring, prognosticating, preventing or treating, or determining the predisposition to, diseases or conditions such as prostate cancer, and for research or forensic science.
XX PS Disclosure; Page 183-184; 100pp; English.
XX CC The present invention relates to novel differentially regulated genes and polypeptides encoded by them. Sequences of the invention are useful in diagnosing, staging, monitoring, prognosticating, preventing, treating or determining the predisposition to diseases or conditions such as prostate cancer. They may be used as molecular markers, drug targets, vaccines, in gene therapy, research, clinical medicine or forensic science. The present sequence is a differentially regulated prostate protein (endothelial monocyte activating polypeptide II), Pc240
XX SQ Sequence 312 AA;
Query Match 100.0%; Score 1573; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 1.6e-135;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MANNDVLRLEQKGAEADQII EYLKQOVSLLEKAILQATLREKKLRVENAKLKKIE 60
Db 1 MANNDVLRLEQKGAEADQII EYLKQOVSLLEKAILQATLREKKLRVENAKLKKIE 60
Qy 61 ELKQELIQAEIQNGVKQIAPPSGTPHANSMVSENVIOSTAVTTVSSGTEQIKGCTGDE 120
Db 61 ELKQELIQAEIQNGVKQIAPPSGTPHANSMVSENVIOSTAVTTVSSGTEQIKGCTGDE 120
Qy 121 KKAKEKIEKGEKKEKQOQSTAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEVD 180
Db 121 KKAKEKIEKGEKKEKQOQSTAGSADSKPIDVSRDLRIGCIITARKHPDADSLYVEVD 180
Qy 181 VGEIAPRTVSVGLVNHVPLEQMNRMVILLCNLKPAGKRGVLSQAMVNCASSPEKIEILA 240
Db 181 VGEIAPRTVSVGLVNHVPLEQMNRMVILLCNLKPAGKRGVLSQAMVNCASSPEKIEILA 240
Qy 241 PPGSVPGDRITFDAPFGEPEKELNPKKKIWEQIQPDLHTNDECVATYKGVPPFVKGV 300
Db 241 PPGSVPGDRITFDAPFGEPEKELNPKKKIWEQIQPDLHTNDECVATYKGVPPFVKGV 300
Qy 301 CQAQTMNSNGIK 312
Db 301 CQAQTMNSNGIK 312
RESULT 3

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